

# Sequence Listing

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 Gerritsen, Mary E.  
 Goddard, Audrey  
 Godowski, Paul J.  
 Grimaldi, J. Christopher  
 Gurney, Austin L.  
 Kljavin, Ivar J.  
 Napier, Mary A.  
 Pan, James  
 Paoni, Nicholas F.  
 Roy, Margaret Ann  
 Stewart, Timothy A.  
 Tumas, Daniel  
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 aactgcgttc tggctaacac tgttgacact gaccacact gaatgtagtc 1050  
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 ccacaagttt cactgttctc attcaagtc ttaactgtgt gaagaacaaa 1150  
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 aataacatga ttttaggttg aaatggcttt agaactattt gggtttgagg 2100  
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 <211> 251  
 <212> FRT  
 <213> Homo sapiens

<400> 6  
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 Arg Tyr Trp Phe Ala Ala Thr Val Ala Val Pro Leu Val Gly Lys  
 20 25 30  
 Leu Gly Leu Ile Ser Pro Ala Tyr Leu Phe Leu Trp Pro Glu Ala  
 35 40 45  
 Phe Leu Tyr Arg Phe Gln Ile Trp Arg Pro Ile Thr Ala Thr Phe  
 50 55 60  
 Tyr Phe Pro Val Gly Pro Gly Thr Gly Phe Leu Tyr Leu Val Asn  
 65 70 75  
 Leu Tyr Phe Leu Tyr Gln Tyr Ser Thr Arg Leu Glu Thr Gly Ala  
 80 85 90  
 Phe Asp Gly Arg Pro Ala Asp Tyr Leu Phe Met Leu Leu Phe Asn  
 95 100 105

Trp	Ile	Cys	Ile	Val	Ile	Thr	Gly	Leu	Ala	Met	Asp	Met	Gln	Leu
				110					115					120
Leu	Met	Ile	Pro	Leu	Ile	Met	Ser	Val	Leu	Tyr	Val	Trp	Ala	Gln
				125					130					135
Leu	Asn	Arg	Asp	Met	Ile	Val	Ser	Phe	Trp	Phe	Gly	Thr	Arg	Phe
				140					145					150
Lys	Ala	Cys	Tyr	Leu	Pro	Trp	Val	Ile	Leu	Gly	Phe	Asn	Tyr	Ile
				155					160					165
Ile	Gly	Gly	Ser	Val	Ile	Asn	Glu	Leu	Ile	Gly	Asn	Leu	Val	Gly
				170					175					180
His	Leu	Tyr	Phe	Phe	Leu	Met	Phe	Arg	Tyr	Pro	Met	Asp	Leu	Gly
				185					190					195
Gly	Arg	Asn	Phe	Leu	Ser	Thr	Pro	Gln	Phe	Leu	Tyr	Arg	Trp	Leu
				200					205					210
Pro	Ser	Arg	Arg	Gly	Gly	Val	Ser	Gly	Phe	Gly	Val	Pro	Pro	Ala
				215					220					225
Ser	Met	Arg	Arg	Ala	Ala	Asp	Gln	Asn	Gly	Gly	Gly	Gly	Arg	His
				230					235					240
Asn	Trp	Gly	Gln	Gly	Phe	Arg	Leu	Gly	Asp	Gln				
				245					250					

<210> 7  
 <211> 1373  
 <212> DNA  
 <213> Homo sapiens

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 ctcttccctc actccctctc ggctccttgt ggcccaaagg cctaaccggg 150  
 gtccggcggt ctggcctagg gatcttcccc gtggccctt tggggcggga 200  
 tggctgcgga agaagaagac gaggtggagt gggtagtgga gagcatcgcg 250  
 gggttctcgc gaggccaga ctggtccatc ccatcttg aatttgtgga 300  
 acagaaatgt gaagttaact gcaaaggagg gcatgtgata actccaggaa 350  
 gccagagacc ggtgattttg gtggcctgtg ttcccttgt ttttgatgat 400  
 gaagaagaaa gcaaatgac ctatacagag attcatcagg aatacaaaga 450  
 actagttaga aagctgttag aagggtacct caaagaaatt ggaattaatg 500  
 aagatcaatt tcaagaagca tgcaattctc ctcttgcaaa gaccatata 550  
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 gaataattca agagagaaat ggtgtattac ctgactgctt aaccgatggc 700

tctgatgtgg tcagtgacct tgaacacgaa gagatgaaaa tcttgagggga 750  
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 ggaaaaaaca gttatcagag gctaaaaacag aagagccac agtgattcc 850  
 agtgaagctg caataatgaa taattcccaa ggggatgggtg aacattttgc 900  
 acaccacccc tcagaagtta aaatgcattt tgctaatacag tcaatagaac 950  
 ctttgggaag aaaagtggaa aggtctgaaa cttcctccct cccacaaaaa 1000  
 ggctgaaga ttcttggtt agagcatgcg agcattgaag gaccaatagc 1050  
 aaacttatca gtacttgaa cagaagaact tcggcaacga gaacactatc 1100  
 tcaagcagaa gagagataag ttgatgtcca tgagaaagga tatgaggact 1150  
 aaacagatac aaaatatgga gcagaaagga aaacccactg gggaggtaga 1200  
 ggaaatgaca gagaaaccag aaatgacagc agaggagaag caaacattac 1250  
 taaagaggag attgcttgca gagaaactca aagaagaagt tattaataag 1300  
 taataattaa gaacaattta aaaaaatgga agttcaaatt gtcttaaaaa 1350  
 taaattattt agtccttaca ctg 1373

<210> 8

<211> 367

<212> PRT

<213> Homo sapiens

<400> 8

Met Ala Ala Glu Glu Glu Asp Glu Val Glu Trp Val Val Glu Ser  
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Ile Ala Gly Phe Leu Arg Gly Pro Asp Trp Ser Ile Pro Ile Leu  
 20 25 30

Asp Phe Val Glu Gln Lys Cys Glu Val Asn Cys Lys Gly Gly His  
 35 40 45

Val Ile Thr Pro Gly Ser Pro Glu Pro Val Ile Leu Val Ala Cys  
 50 55 60

Val Pro Leu Val Phe Asp Asp Glu Glu Glu Ser Lys Leu Thr Tyr  
 65 70 75

Thr Glu Ile His Gln Glu Tyr Lys Glu Leu Val Glu Lys Leu Leu  
 80 85 90

Glu Gly Tyr Leu Lys Glu Ile Gly Ile Asn Glu Asp Gln Phe Gln  
 95 100 105

Glu Ala Cys Thr Ser Pro Leu Ala Lys Thr His Thr Ser Gln Ala  
 110 115 120

Ile Leu Gln Pro Val Leu Ala Ala Glu Asp Phe Thr Ile Phe Lys  
 125 130 135

Ala Met Met Val Gln Lys Asn Ile Glu Met Gln Leu Gln Ala Ile  
 140 145 150

Arg	Ile	Ile	Gln	Glu	Arg	Asn	Gly	Val	Leu	Pro	Asp	Cys	Leu	Thr	155	160	165
Asp	Gly	Ser	Asp	Val	Val	Ser	Asp	Leu	Glu	His	Glu	Glu	Met	Lys	170	175	180
Ile	Leu	Arg	Glu	Val	Leu	Arg	Lys	Ser	Lys	Glu	Glu	Tyr	Asp	Gln	185	190	195
Glu	Glu	Glu	Arg	Lys	Arg	Lys	Lys	Gln	Leu	Ser	Glu	Ala	Lys	Thr	200	205	210
Glu	Glu	Pro	Thr	Val	His	Ser	Ser	Glu	Ala	Ala	Ile	Met	Asn	Asn	215	220	225
Ser	Gln	Gly	Asp	Gly	Glu	His	Phe	Ala	His	Pro	Pro	Ser	Glu	Val	230	235	240
Lys	Met	His	Phe	Ala	Asn	Gln	Ser	Ile	Glu	Pro	Leu	Gly	Arg	Lys	245	250	255
Val	Glu	Arg	Ser	Glu	Thr	Ser	Ser	Leu	Pro	Gln	Lys	Gly	Leu	Lys	260	265	270
Ile	Pro	Gly	Leu	Glu	His	Ala	Ser	Ile	Glu	Gly	Pro	Ile	Ala	Asn	275	280	285
Leu	Ser	Val	Leu	Gly	Thr	Glu	Glu	Leu	Arg	Gln	Arg	Glu	His	Tyr	290	295	300
Leu	Lys	Gln	Lys	Arg	Asp	Lys	Leu	Met	Ser	Met	Arg	Lys	Asp	Met	305	310	315
Arg	Thr	Lys	Gln	Ile	Gln	Asn	Met	Glu	Gln	Lys	Gly	Lys	Pro	Thr	320	325	330
Gly	Glu	Val	Glu	Glu	Met	Thr	Glu	Lys	Pro	Glu	Met	Thr	Ala	Glu	335	340	345
Glu	Lys	Gln	Thr	Leu	Leu	Lys	Arg	Arg	Leu	Leu	Ala	Glu	Lys	Leu	350	355	360
Lys	Glu	Glu	Val	Ile	Asn	Lys									365		

<210> 9  
 <211> 418  
 <212> DNA  
 <213> Homo sapiens

<400> 9  
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 aaggttacct caaagaaatt ggaattaatg aagatcaatt tcaagaagca 150  
 tgcacttctc ctcttgcaaa gaccataaca tcacaggcca tttttgcaac 200  
 ctgtgtttggc agcagaagat ttactatct ttaaagcaat gatggtccag 250  
 aaaaacattg aaatgcagct gcaagccatt cgaataattc aagagagaaa 300

tggtgtatta cctgactgct taaccgatgg ctctgatgtg gtcagtgacc 350  
ttgaacacga agagatgaaa atcctgaggg aagttcttag aaaatcaaaa 400  
gaggaatatg accaggaa 418

<210> 10  
<211> 22  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe

<400> 10  
ttgacctata cagagattca tc 22

<210> 11  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 11  
ctaagaactt ccctcaggat ttt 23

<210> 12  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 12  
atgaagatca atttcaagaa gcatgcactt ctccctcttg 40

<210> 13  
<211> 2886  
<212> DNA  
<213> Homo sapiens

<400> 13  
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tactacgggg ctagacagtt actgtctcag ctctaggatg tgcgttcttc 150  
cactagaagc tcttctgagg gaggttaatta aaaaacagtg gaatggaaaa 200  
acagtgtctg agtcacacctg taatatgctc ctgtgaaca atgtatacat 250  
tctctgctag tgccatatcc attgctttaa gctcaagtcg catcttacta 300  
gtgaagtatt ctgccaatga agaaaacaag tatgattatc ttccaactac 350  
tgtgaatgtg tgcgcagaac tggatgaagct agttttctgt gtgcttgtgt 400  
cattctgtgt tataaagaaa gatcatcaaa gtagaaattt gaaatatgct 450



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 ttatttctctg gataaactga ttgtcttcta tgtcctgtcc tatcttcaac 550  
 cagccatggc tgttatcttc tcaaatttta gcattataac aacagctctt 600  
 ctattcagga tagtgctgaa gaggcgtcta aactggatcc agtgggcttc 650  
 cctcctgact ttatttttgt ctattgtggc ctgactgcc gggactaaaa 700  
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 totgtctcc tttctcctaa gtttcatgca gatgaatata aggtaatata 2800  
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 tgggtgaaat ttgtaattaa aataattatt aaacct 2886

<210> 14  
 <211> 424  
 <212> PRT  
 <213> Homo sapiens

<400> 14  
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 Thr Met Tyr Thr Phe Leu Leu Gly Ala Ile Phe Ile Ala Leu Ser  
 20 25 30  
 Ser Ser Arg Ile Leu Leu Val Lys Tyr Ser Ala Asn Glu Glu Asn  
 35 40 45  
 Lys Tyr Asp Tyr Leu Pro Thr Thr Val Asn Val Cys Ser Glu Leu  
 50 55 60  
 Val Lys Leu Val Phe Cys Val Leu Val Ser Phe Cys Val Ile Lys  
 65 70 75  
 Lys Asp His Gln Ser Arg Asn Leu Lys Tyr Ala Ser Trp Lys Glu  
 80 85 90  
 Phe Ser Asp Phe Met Lys Trp Ser Ile Pro Ala Phe Leu Tyr Phe  
 95 100 105  
 Leu Asp Asn Leu Ile Val Phe Tyr Val Leu Ser Tyr Leu Gln Pro  
 110 115 120

Ala Met Ala Val	Ile Phe Ser Asn Phe Ser	Ile Ile Thr Thr	Ala
	125	130	135
Leu Leu Phe Arg	Ile Val Leu Lys Arg Arg	Leu Asn Trp Ile	Gln
	140	145	150
Trp Ala Ser Leu	Leu Thr Leu Phe Leu Ser	Ile Val Ala Leu Thr	
	155	160	165
Ala Gly Thr Lys	Thr Leu Gln His Asn Leu	Ala Gly Arg Gly	Phe
	170	175	180
His His Asp Ala	Phe Phe Ser Pro Ser Asn Ser	Cys Leu Leu Phe	
	185	190	195
Arg Ser Glu Cys	Pro Arg Lys Asp Asn Cys	Thr Ala Lys Glu Trp	
	200	205	210
Thr Phe Pro Glu	Ala Lys Trp Asn Thr Thr	Ala Arg Val Phe Ser	
	215	220	225
His Ile Arg Leu	Gly Met Gly His Val Leu	Ile Ile Val Gln Cys	
	230	235	240
Phe Ile Ser Ser	Met Ala Asn Ile Tyr Asn	Glu Lys Ile Leu Lys	
	245	250	255
Glu Gly Asn Gln	Leu Thr Glu Ser Ile Phe	Ile Gln Asn Ser Lys	
	260	265	270
Leu Tyr Phe Phe	Gly Ile Leu Phe Asn Gly	Leu Thr Leu Gly Leu	
	275	280	285
Gln Arg Ser Asn	Arg Asp Gln Ile Lys Asn	Cys Gly Phe Phe Tyr	
	290	295	300
Gly His Ser Ala	Phe Ser Val Ala Leu Ile	Phe Val Thr Ala Phe	
	305	310	315
Gln Gly Leu Ser	Val Ala Phe Ile Leu Lys	Phe Leu Asp Asn Met	
	320	325	330
Phe His Val Leu	Met Ala Gln Val Thr Thr	Val Ile Ile Thr Thr	
	335	340	345
Val Ser Val Leu	Val Phe Asp Phe Arg Pro	Ser Leu Glu Phe Phe	
	350	355	360
Leu Glu Ala Pro	Ser Val Leu Leu Ser Ile	Phe Ile Tyr Asn Ala	
	365	370	375
Ser Lys Pro Gln	Val Pro Glu Tyr Ala Pro	Arg Gln Glu Arg Ile	
	380	385	390
Arg Asp Leu Ser	Gly Asn Leu Trp Glu Arg	Ser Ser Gly Asp Gly	
	395	400	405
Glu Glu Leu Glu	Arg Leu Thr Lys Pro Lys	Ser Asp Glu Ser Asp	
	410	415	420
Glu Asp Thr Phe			

<210> 15  
<211> 755  
<212> DNA  
<213> Homo sapiens

<400> 15  
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tactacgggg ctagacagtt actgtctcag ctctaggatg tgcgttcttc 200  
cactagaagc tcttctgagg gaggtaatta aaaaacagtg gaatggaaaa 250  
acagtgcctg agtcatcctg taatatgctc ctgtcaaca atgtatacat 300  
tctgctagtg tgccatattc attgctttta gctcaagtcg catcttacta 350  
gtgaagtatt ctgccaatga agaaaacaag tatgattatc ttccaactac 400  
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cattctgtgt tataaagaaa gatcatcaaa gtagaaattt gaaatatgct 500  
tcttggaagg aattctctga ttcatgaag tggccattc ctgcctttct 550  
ttatttctcg gataacttga ttgtcttcta tgtcctgtcc tatcttcaac 600  
cagccatggc tgttatcttc tcaaatttta gcattataac aacagctctt 650  
ctattcagga tagtgctgaa gaggcgtcta aactggatcc agtgggcttc 700  
cctcctgact ttatttttgt ctattgtggc ctgactgcc gggactaaaa 750  
cttta 755

<210> 16  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 16  
ctatacctac tgtagcttct 20

<210> 17  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 17  
tcagagaatt ccttcagga 20

<210> 18  
<211> 40  
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 18

acagtgtgtg agtcatcctg taatatgctc ctgtcaaca 40

<210> 19

<211> 2142

<212> DNA

<213> Homo sapiens

<400> 19

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cgcgcgcgcg cctgggctaa ggctgctacg aagcgagctt gggaggagca 100  
gcggcctcgc gggcagagga gcatcccgct taccaggctc caagcgcgct 150  
ggcccgcgcg tcatggccaa aggagaaggc gccgagagcg gctccgcgcc 200  
ggggctgcta ccaccagca tctccaaag cactgaacgc cgggccagg 250  
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<210> 20  
 <211> 458  
 <212> PRT  
 <213> Homo sapiens

<400> 20  
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 Trp Ala Glu Pro Gly Met Pro Ser Gln Thr Pro Trp Trp Ala Ser  
 20 25 30  
 Ala Ser Ala Asn Pro Pro Gly Pro Ala Trp Val Ala Leu Cys Pro  
 35 40 45  
 Gly Ser Ser Ser Pro Arg Pro Trp Pro Ser Leu Pro Thr Ser Ser  
 50 55 60  
 Ser Gly Ser Cys Pro Thr Ser His Thr Ala Arg Pro Ile Gly Thr  
 65 70 75  
 Cys Phe Ser Ile Ala Ser Leu Lys Gln Trp Ser Arg Val Ser Met  
 80 85 90  
 Phe Pro Thr Arg Leu Ser Pro Cys Ser Ser Ala Thr Glu Gln Thr  
 95 100 105

Glu Arg Asp Ser	Ala Thr Ala Tyr Arg	Met Thr Val Glu Val Leu
110		115 120
Gly Thr Val Leu	Gly Thr Ala Ile Gln Gly Gln Ile Val Gly Gln	
125		130 135
Ala Asp Thr Pro Cys Phe Gln Asp Phe Asn Ser Ser Thr Val Ala		
140		145 150
Ser Gln Ser Ala Asn His Thr His Gly Thr Thr Ser His Arg Glu		
155		160 165
Thr Gln Lys Ala Tyr Leu Leu Ala Ala Gly Val Ile Val Cys Ile		
170		175 180
Tyr Ile Ile Cys Ala Val Ile Leu Ile Leu Gly Val Arg Glu Gln		
185		190 195
Arg Glu Pro Tyr Glu Ala Gln Gln Ser Glu Pro Ile Ala Tyr Phe		
200		205 210
Arg Gly Leu Arg Leu Val Met Ser His Gly Pro Tyr Ile Lys Leu		
215		220 225
Ile Thr Gly Phe Leu Phe Thr Ser Leu Ala Phe Met Leu Val Glu		
230		235 240
Gly Asn Phe Val Leu Phe Cys Thr Tyr Thr Leu Gly Phe Arg Asn		
245		250 255
Glu Phe Gln Asn Leu Leu Leu Ala Ile Met Leu Ser Ala Thr Leu		
260		265 270
Thr Ile Pro Ile Trp Gln Trp Phe Leu Thr Arg Phe Gly Lys Lys		
275		280 285
Thr Ala Val Tyr Val Gly Ile Ser Ser Ala Val Pro Phe Leu Ile		
290		295 300
Leu Val Ala Leu Met Glu Ser Asn Leu Ile Ile Thr Tyr Ala Val		
305		310 315
Ala Val Ala Ala Gly Ile Ser Val Ala Ala Phe Leu Leu Pro		
320		325 330
Trp Ser Met Leu Pro Asp Val Ile Asp Asp Phe His Leu Lys Gln		
335		340 345
Pro His Phe His Gly Thr Glu Pro Ile Phe Phe Ser Phe Tyr Val		
350		355 360
Phe Phe Thr Lys Phe Ala Ser Gly Val Ser Leu Gly Ile Ser Thr		
365		370 375
Leu Ser Leu Asp Phe Ala Gly Tyr Gln Thr Arg Gly Cys Ser Gln		
380		385 390
Pro Glu Arg Val Lys Phe Thr Leu Asn Met Leu Val Thr Met Ala		
395		400 405
Pro Ile Val Leu Ile Leu Leu Gly Leu Leu Leu Phe Lys Met Tyr		
410		415 420

Pro Ile Asp Glu Glu Arg Arg Arg Gln Asn Lys Lys Ala Leu Gln  
425 430 435

Ala Leu Arg Asp Glu Ala Ser Ser Ser Gly Cys Ser Glu Thr Asp  
440 445 450

Ser Thr Glu Leu Ala Ser Ile Leu  
455

<210> 21  
<211> 571  
<212> DNA  
<213> Homo sapiens

<400> 21  
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accctatgaa gccacgagct ctgagccaat cgccactctc cggggcctac 150  
ggctgtgcat gagccacggc ccatacatca aactatttac tggcttcttc 200  
ttcactctct tggctttcat gctgggtggag gggaactttg tcttgttttg 250  
cacctacacc ttgggcttcc gcaatgaatt ccagaatcta ctccctggcca 300  
tcatgtctct ggccacttta accattccca tctggcagtg gttcttgacc 350  
cggtttggca agaagacagc tgtatatgtt gggatctcat cagcagtgcc 400  
attctctcat ttgggtggcc tcatggagag taacctcatc attacatgat 450  
cggtagctgt ggcagctggc atcagtggtg cagctgcctt ctactaacc 500  
tggtcctatg tgcctgatgt cattgaagac ttccatctga agcagcccca 550  
cttccatgga accgagccca t 571

<210> 22  
<211> 1173  
<212> DNA  
<213> Homo sapiens

<400> 22  
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aaagggtcag gtatgagcag gtctgaagac taacattttg tgaagtgtga 100  
aaacagaaaa cctgttagaa atgtgtgtgt ttacgcaagg cctcagtttc 150  
cttccttcag cccttgtaat ttggacatct gctgctttca tattttcata 200  
cattactgca gtaacactcc accatataga cccggtttta ctttatatca 250  
gtgacactgg tacagtagct ccagaaaaat gcttatttgg ggcaatgcta 300  
aatattgcgg cagttttatg cattgctacc atttatgttc gttataagca 350  
agttcatgct ctgagtcctg aagagaacgt tatcatcaaa ttaaacaagg 400  
ctggccttgt acttgaata ctgagttgtt taggactttc tattgtggca 450



aacttcaga aaacaaccct tttgtctgca catgtaagtg gagctgtgct 500  
taccttttgt atgggctcat tatatatgtt tgttcagacc atcctttcct 550  
accaaatgca gcccaaaatc catggcaaac aagtcttctg gatcagactg 600  
ttgttggtta tctggtgtgg agtaagtgca cttagcatgc tgacttgtc 650  
atcagttttg cacagtggca attttgggac tgatttagaa cagaaactcc 700  
attggaaccc cgaggacaaa ggttatgtgc ttcacatgat cactactgca 750  
gcagaatggt ctatgtcatt ttcttctttt ggttttttcc tgacttacat 800  
tcgtgatttt cagaaaattt ctttacgggt ggaagccaat ttacatggat 850  
taacctctta tgacactgca ccttgcccta ttaacaatga acgaacacgg 900  
ctactttcca gagatatattg atgaaaggat aaaatatctt tgtaatgatt 950  
atgattctca gggattgggg aaaggttcac agaagttgct tattctctc 1000  
tgaaattttc aaccacttaa tcaaggctga cagtaacact gatgaatgct 1050  
gataatcagg aaacatgaaa gaagccattt gatagattat tctaaaggat 1100  
atcatcaaga agactattaa aaacacctat gcctatactt ttttatctca 1150  
gaaaataaag tcaaaagact atg 1173

<210> 23

<211> 266

<212> PRT

<213> Homo sapiens

<400> 23

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Val	Ile	Trp	Thr	Ser	Ala	Ala	Phe	Ile	Phe	Ser	Tyr	Ile	Thr	Ala
				20						25				30
Val	Thr	Leu	His	His	Ile	Asp	Pro	Ala	Leu	Pro	Tyr	Ile	Ser	Asp
				35						40				45
Thr	Gly	Thr	Val	Ala	Pro	Glu	Lys	Cys	Leu	Phe	Gly	Ala	Met	Leu
				50						55				60
Asn	Ile	Ala	Ala	Val	Leu	Cys	Ile	Ala	Thr	Ile	Tyr	Val	Arg	Tyr
				65						70				75
Lys	Gln	Val	His	Ala	Leu	Ser	Pro	Glu	Glu	Asn	Val	Ile	Ile	Lys
				80						85				90
Leu	Asn	Lys	Ala	Gly	Leu	Val	Leu	Gly	Ile	Leu	Ser	Cys	Leu	Gly
				95						100				105
Leu	Ser	Ile	Val	Ala	Asn	Phe	Gln	Lys	Thr	Thr	Leu	Phe	Ala	Ala
				110						115				120
His	Val	Ser	Gly	Ala	Val	Leu	Thr	Phe	Gly	Met	Gly	Ser	Leu	Tyr
				125						130				135

Met Phe Val Gln Thr Ile Leu Ser Tyr Gln Met Gln Pro Lys Ile  
140 145 150

His Gly Lys Gln Val Phe Trp Ile Arg Leu Leu Leu Val Ile Trp  
155 160 165

Cys Gly Val Ser Ala Leu Ser Met Leu Thr Cys Ser Ser Val Leu  
170 175 180

His Ser Gly Asn Phe Gly Thr Asp Leu Glu Gln Lys Leu His Trp  
185 190 195

Asn Pro Glu Asp Lys Gly Tyr Val Leu His Met Ile Thr Thr Ala  
200 205 210

Ala Glu Trp Ser Met Ser Phe Ser Phe Phe Gly Phe Phe Leu Thr  
215 220 225

Tyr Ile Arg Asp Phe Gln Lys Ile Ser Leu Arg Val Glu Ala Asn  
230 235 240

Leu His Gly Leu Thr Leu Tyr Asp Thr Ala Pro Cys Pro Ile Asn  
245 250 255

Asn Glu Arg Thr Arg Leu Leu Ser Arg Asp Ile  
260 265

<210> 24  
<211> 485  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 14, 484  
<223> unknown base

<400> 24  
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gagcggagat cctcaaacgg cctagtgttt cgcgcttccg gagaaaatca 150  
gggtgtctat taattcctct gggttggtga agcagttacc aagaatcttc 200  
aacccctttc cacaaaagct aattgagtac acgttctctg tgagtacaag 250  
ttctgttgta ttacaaaag gtgcaggtat gagcaggtct gaagactaac 300  
atattgtgaa gttgtaaaac agaaaacctg ttagaatgt ggtggtttca 350  
gcaaggccct agtttccttc cttcagccct tgtaattgg acatctgctg 400  
ctttcatatt ttcatacatt actgcagtaa cactccacca tatagaccog 450  
gctttacott atatcagtga cactgtgata gtanc 485

<210> 25  
<211> 40  
<212> DNA  
<213> Artificial Sequence

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<220>
<223> Synthetic oligonucleotide probe

<400> 25
acctgttaga aatgtggtgg ttccagcaag gcctcagttt 40

<210> 26
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
ggagatagct gctatgggtt cttcaggcac aacttaacat gggaag 46

<210> 27
<211> 1399
<212> DNA
<213> Homo sapiens

<400> 27
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ctgcccgcgc ggcgggggtg cggagccgac atgcgccgcg ttctoggcct 100
ccttctggtc ttgcgcggtc gcaccttcgc ctgtacttg ctgtcgacgc 150
gactgcgccg cgggcgagga ctgggctcca ccgaggaggc tggaggcagg 200
tcgctgtggt tccctccga cctggcagag ctgcgggagc tctctgaggt 250
ccttcgagag taccggaagg agcaccaggc ctacgtgttc ctgctcttct 300
ggggcgccct cctctacaaa cagggccttg ccatcccgcg ctccagcttc 350
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gtgctgtgtg ttgacctcgg tgggtgccac atgctgctac ctgctctcca 450
gtatttttgg caaacagttg gtggtgtcct actttctcga taaagtggcc 500
ctgctgcaga gaaaggtgga ggagaacaga aacagcttgt ttttttctt 550
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atcggtttga tcccatataa ttcatctgt gtgcagacag ggtccatcct 700
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tatacacagt agaaaagaca catgatctgg attttctgtt tgccacatcc 900
ctggactcag ttgcttattt gtgtaatgga tgtggctctc taaagccctt 950
cattgttttt gattgccttc tataggtgat gtggacactg tgcacatgat 1000

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 gccaggcggtg gtggcaggca cctgtaatcc cagctactcg ggaggctgag 1300  
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 cacaccactg cactccagcc tgggtgatag agtgagacac tgtcttgac 1399

<210> 28  
 <211> 264  
 <212> PRT  
 <213> Homo sapiens

<400> 28  
 Met Arg Pro Leu Leu Gly Leu Leu Leu Val Phe Ala Gly Cys Thr  
 1 5 10 15  
 Phe Ala Leu Tyr Leu Leu Ser Thr Arg Leu Pro Arg Gly Arg Arg  
 20 25 30  
 Leu Gly Ser Thr Glu Glu Ala Gly Gly Arg Ser Leu Trp Phe Pro  
 35 40 45  
 Ser Asp Leu Ala Glu Leu Arg Glu Leu Ser Glu Val Leu Arg Glu  
 50 55 60  
 Tyr Arg Lys Glu His Gln Ala Tyr Val Phe Leu Leu Phe Cys Gly  
 65 70 75  
 Ala Tyr Leu Tyr Lys Gln Gly Phe Ala Ile Pro Gly Ser Ser Phe  
 80 85 90  
 Leu Asn Val Leu Ala Gly Ala Leu Phe Gly Pro Trp Leu Gly Leu  
 95 100 105  
 Leu Leu Cys Cys Val Leu Thr Ser Val Gly Ala Thr Cys Cys Tyr  
 110 115 120  
 Leu Leu Ser Ser Ile Phe Gly Lys Gln Leu Val Val Ser Tyr Phe  
 125 130 135  
 Pro Asp Lys Val Ala Leu Leu Gln Arg Lys Val Glu Glu Asn Arg  
 140 145 150  
 Asn Ser Leu Phe Phe Phe Leu Leu Phe Leu Arg Leu Phe Pro Met  
 155 160 165  
 Thr Pro Asn Trp Phe Leu Asn Leu Ser Ala Pro Ile Leu Asn Ile  
 170 175 180  
 Pro Ile Val Gln Phe Phe Phe Ser Val Leu Ile Gly Leu Ile Pro  
 185 190 195  
 Tyr Asn Phe Ile Cys Val Gln Thr Gly Ser Ile Leu Ser Thr Leu  
 200 205 210

Thr Ser Leu Asp Ala Leu Phe Ser Trp Asp Thr Val Phe Lys Leu  
 215 220  
 Leu Ala Ile Ala Met Val Ala Leu Ile Pro Gly Thr Leu Ile Lys  
 230 235 240  
 Lys Phe Ser Gln Lys His Leu Gln Leu Asn Glu Thr Ser Thr Ala  
 245 250 255  
 Asn His Ile His Ser Arg Lys Asp Thr  
 260

<210> 29  
 <211> 1292  
 <212> DNA  
 <213> Homo sapiens

<400> 29  
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 ggtttccgaa ctgccagctc agaataggaa aataacttgg gattttatat 150  
 tggaagacat ggaatcttgc gccaacgaga tcagcattta tgacaaactt 200  
 tcagagactg ttgatttggg gagacagacc ggccatcagt gtggcatgtc 250  
 agagaaggca attgaaaaa ttatcagaca gctgctggaa aagaatgaac 300  
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 tttcagccca ttgacacctg agccagtgtc ttctggagct cacacctggc 450  
 gctcactcat ccatcacatt aggctgatgt ccttgcccat tgccaagaag 500  
 tacatgtcag aaaataaggg agttcctctg catgggggtg atgaagacag 550  
 accctttcca gactttgacc cctgggtggac aaacgactgt gagcagaatg 600  
 agtcagagcc cattcctgcc aactgcactg gctgtgccca gaaacacctg 650  
 aaggtgatgc tcctggaaga cgcccaagg aaatttgaga ggctccatcc 700  
 actggtgatc aagacgggaa agcccctgtt ggaggaagag attcagcatt 750  
 ttttgtgccg gtaccctgag gcgacagaag gcttctctga aggggttttc 800  
 gccaaagtgt ggcgctgctt tcctgagcgg tggttcccat ttccattacc 850  
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 tttcttcacc cagaacctgt tgtggggagt aagatgcata agatgcctga 1000  
 cctattttatc attggcagcg gtgaggccat gttgcagctc atccctccct 1050  
 tccagtgccg aagacattgt cagtctgtgg ccattgccaat agagccaggg 1100  
 gatatcggtc atgtcgacac caccactggg aaggtctaac ttatagccag 1150

aggggtccag cctttggtca tctgcgatgg aaccgctttc tcagaactgt 1200  
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 gaaaggggaa aaataaaaac aaaaacgatg aaactgcaaa aa 1292

<210> 30  
 <211> 347  
 <212> PRT  
 <213> Homo sapiens

<400> 30  
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 20 25 30  
 Ser Glu Lys Ala Ile Glu Lys Phe Ile Arg Gln Leu Leu Glu Lys  
 35 40 45  
 Asn Glu Pro Gln Arg Pro Pro Pro Gln Tyr Pro Leu Leu Ile Val  
 50 55 60  
 Val Tyr Lys Val Leu Ala Thr Leu Gly Leu Ile Leu Leu Thr Ala  
 65 70 75  
 Tyr Phe Val Ile Gln Pro Phe Ser Pro Leu Ala Pro Glu Pro Val  
 80 85 90  
 Leu Ser Gly Ala His Thr Trp Arg Ser Leu Ile His His Ile Arg  
 95 100 105  
 Leu Met Ser Leu Pro Ile Ala Lys Lys Tyr Met Ser Glu Asn Lys  
 110 115 120  
 Gly Val Pro Leu His Gly Gly Asp Glu Asp Arg Pro Phe Pro Asp  
 125 130 135  
 Phe Asp Pro Trp Trp Thr Asn Asp Cys Glu Gln Asn Glu Ser Glu  
 140 145 150  
 Pro Ile Pro Ala Asn Cys Thr Gly Cys Ala Gln Lys His Leu Lys  
 155 160 165  
 Val Met Leu Leu Glu Asp Ala Pro Arg Lys Phe Glu Arg Leu His  
 170 175 180  
 Pro Leu Val Ile Lys Thr Gly Lys Pro Leu Leu Glu Glu Ile  
 185 190 195  
 Gln His Phe Leu Cys Gln Tyr Pro Glu Ala Thr Glu Gly Phe Ser  
 200 205 210  
 Glu Gly Phe Phe Ala Lys Trp Trp Arg Cys Phe Pro Glu Arg Trp  
 215 220 225  
 Phe Pro Phe Pro Tyr Pro Trp Arg Arg Pro Leu Asn Arg Ser Gln  
 230 235 240  
 Met Leu Arg Glu Leu Phe Pro Val Phe Thr His Leu Pro Phe Pro  
 245 250 255

Lys Asp Ala Ser Leu Asn Lys Cys Ser Phe Leu His Pro Glu Pro  
 260 265 270  
 Val Val Gly Ser Lys Met His Lys Met Pro Asp Leu Phe Ile Ile  
 275 280 285  
 Gly Ser Gly Glu Ala Met Leu Gln Leu Ile Pro Pro Phe Gln Cys  
 290 295 300  
 Arg Arg His Cys Gln Ser Val Ala Met Pro Ile Glu Pro Gly Asp  
 305 310 315  
 Ile Gly Tyr Val Asp Thr Thr His Trp Lys Val Tyr Val Ile Ala  
 320 325 330  
 Arg Gly Val Gln Pro Leu Val Ile Cys Asp Gly Thr Ala Phe Ser  
 335 340 345  
 Glu Leu

<210> 31  
 <211> 478  
 <212> DNA  
 <213> Homo sapiens

<400> 31  
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 gcccgagggg cgcgagcccc gcatgaatca ttgtagtcaa tcattttcca 100  
 gttctcagcc gttcagttgt gatcaaggga cactgggttt ccgaactgcc 150  
 agctcagaat aggaaaataa cttgggattt tatattggaa gacatggatc 200  
 ttgctgcca cgagatcagc atttatgaca aactttcaga gactgttgat 250  
 ttggtgagac agaccggcca tcagtgtggc atgtcagaga aggcaattga 300  
 aaaatttata agacagctgc tggaaaagaa tgaacctcag agaccccccc 350  
 cgcagtatcc tctccttata gttgtgtata aggttctcgc aaccttggga 400  
 ttaattctgc tcaactgcta ctttgtgatt caacctttca gccattagc 450  
 acctgagcca gtgctttgtg gagctcac 478

<210> 32  
 <211> 3531  
 <212> DNA  
 <213> Homo sapiens

<400> 32  
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 gcagagcgct gctcctggct ggtgccactg gtgcgcagc tgctagaccg 150  
 tgctatagag ccgctggggc tcagtgaggg actgccctcc ctgccaccca 200  
 ccaatggcag cccacacctt tttgaagact tccaggcttt ttgtgccaca 250

cccgaatggc gccacttcat cgacaaacag gtacagccaa ccatgtccca 300  
 gttcgaatg gacacgtatg ctaagagcca cgacctatg tcaggtttct 350  
 ggaatgcctg ctatgacatg cttatgagca gtgggcagcg gcgccagtgg 400  
 gagcgcgccc agagtcgtcg ggccctccag gagctggtgc tggaacctgc 450  
 gcagaggcgg gcgcgcctgg aggggctacg ctacacggca gtgctgaagc 500  
 agcaggcaac gcagcactcc atggccctgc tgcactgggg ggcgctgtgg 550  
 cgccagctcg ccagcccatg tggggcctgg gcgctgaggg acactcccat 600  
 cccccgctgg aaactgtcca gcgccgagac atattcacgc atgcgtctga 650  
 agctggtgcc caaccatcac ttcagccctc acctggaagc cagcgtcttc 700  
 cgagacaate tgggtgaggt tccctgaca cccaccgagg aggcctcact 750  
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 cgagtgcgag ctggtgacgg tagtggcgtt ggtcccagg ctgctggagg 950  
 tcaccacaca gaatgtatac ttctacgatg gcagcactga gcgcgtggaa 1000  
 accgaggagg gcatcggcta tgatttcgg cgcccactgg cccagctgcg 1050  
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 gcctacggcc cccctctcaa ggctacctaa gcagccgctc ccccaggag 1300  
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 ctctctggag aaccagaacg gttttgacct gggctgtctc cagctgaacca 1850



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<210> 33  
 <211> 1003  
 <212> PRT  
 <213> Homo sapiens

<400> 33  
 Met Ser Gln Phe Glu Met Asp Thr Tyr Ala Lys Ser His Asp Leu  
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 Met Ser Gly Phe Trp Asn Ala Cys Tyr Asp Met Leu Met Ser Ser  
 20 25 30  
 Gly Gln Arg Arg Gln Trp Glu Arg Ala Gln Ser Arg Arg Ala Phe  
 35 40 45  
 Gln Glu Leu Val Leu Glu Pro Ala Gln Arg Arg Ala Arg Leu Glu  
 50 55 60  
 Gly Leu Arg Tyr Thr Ala Val Leu Lys Gln Gln Ala Thr Gln His  
 65 70 75  
 Ser Met Ala Leu Leu His Trp Gly Ala Leu Trp Arg Gln Leu Ala  
 80 85 90  
 Ser Pro Cys Gly Ala Trp Ala Leu Arg Asp Thr Pro Ile Pro Arg  
 95 100 105  
 Trp Lys Leu Ser Ser Ala Glu Thr Tyr Ser Arg Met Arg Leu Lys  
 110 115 120  
 Leu Val Pro Asn His His Phe Asp Pro Leu Glu Ala Ser Ala  
 125 130 135  
 Leu Arg Asp Asn Leu Gly Glu Val Pro Leu Thr Pro Thr Glu Glu  
 140 145 150  
 Ala Ser Leu Pro Leu Ala Val Thr Lys Glu Ala Lys Val Ser Thr  
 155 160 165  
 Pro Pro Glu Leu Leu Gln Glu Asp Gln Leu Gly Glu Asp Glu Leu  
 170 175 180  
 Ala Glu Leu Glu Thr Pro Met Glu Ala Ala Glu Leu Asp Glu Gln  
 185 190 195  
 Arg Glu Lys Leu Val Leu Ser Ala Glu Cys Gln Leu Val Thr Val  
 200 205 210  
 Val Ala Val Val Pro Gly Leu Leu Glu Val Thr Thr Gln Asn Val  
 215 220 225  
 Tyr Phe Tyr Asp Gly Ser Thr Glu Arg Val Glu Thr Glu Glu Gly  
 230 235 240  
 Ile Gly Tyr Asp Phe Arg Arg Pro Leu Ala Gln Leu Arg Glu Val  
 245 250 255  
 His Leu Arg Arg Phe Asn Leu Arg Arg Ser Ala Leu Glu Leu Phe  
 260 265 270

Phe	Ile	Asp	Gln	Ala	Asn	Tyr	Phe	Leu	Asn	Phe	Pro	Cys	Lys	Val	275	280	285
Gly	Thr	Thr	Pro	Val	Ser	Ser	Pro	Ser	Gln	Thr	Pro	Arg	Pro	Gln	290	295	300
Pro	Gly	Pro	Ile	Pro	Pro	His	Thr	Gln	Val	Arg	Asn	Gln	Val	Tyr	305	310	315
Ser	Trp	Leu	Leu	Arg	Leu	Arg	Pro	Pro	Ser	Gln	Gly	Tyr	Leu	Ser	320	325	330
Ser	Arg	Ser	Pro	Gln	Glu	Met	Leu	Arg	Ala	Ser	Gly	Leu	Thr	Gln	335	340	345
Lys	Trp	Val	Gln	Arg	Glu	Ile	Ser	Asn	Phe	Glu	Tyr	Leu	Met	Gln	350	355	360
Leu	Asn	Thr	Ile	Ala	Gly	Arg	Thr	Tyr	Asn	Asp	Leu	Ser	Gln	Tyr	365	370	375
Pro	Val	Phe	Pro	Trp	Val	Leu	Gln	Asp	Tyr	Val	Ser	Pro	Thr	Leu	380	385	390
Asp	Leu	Ser	Asn	Pro	Ala	Val	Phe	Arg	Asp	Leu	Ser	Lys	Pro	Ile	395	400	405
Gly	Val	Val	Asn	Pro	Lys	His	Ala	Gln	Leu	Val	Arg	Glu	Lys	Tyr	410	415	420
Glu	Ser	Phe	Glu	Asp	Pro	Ala	Gly	Thr	Ile	Asp	Lys	Phe	His	Tyr	425	430	435
Gly	Thr	His	Tyr	Ser	Asn	Ala	Ala	Gly	Val	Met	His	Tyr	Leu	Ile	440	445	450
Arg	Val	Glu	Pro	Phe	Thr	Ser	Leu	His	Val	Gln	Leu	Gln	Ser	Gly	455	460	465
Arg	Phe	Asp	Cys	Ser	Asp	Arg	Gln	Phe	His	Ser	Val	Ala	Ala	Ala	470	475	480
Trp	Gln	Ala	Arg	Leu	Glu	Ser	Pro	Ala	Asp	Val	Lys	Glu	Leu	Ile	485	490	495
Pro	Glu	Phe	Phe	Tyr	Phe	Pro	Asp	Phe	Leu	Glu	Asn	Gln	Asn	Gly	500	505	510
Phe	Asp	Leu	Gly	Cys	Leu	Gln	Leu	Thr	Asn	Glu	Lys	Val	Gly	Asp	515	520	525
Val	Val	Leu	Pro	Pro	Trp	Ala	Ser	Ser	Pro	Glu	Asp	Phe	Ile	Gln	530	535	540
Gln	His	Arg	Gln	Ala	Leu	Glu	Ser	Glu	Tyr	Val	Ser	Ala	His	Leu	545	550	555
His	Glu	Trp	Ile	Asp	Leu	Ile	Phe	Gly	Tyr	Lys	Gln	Arg	Gly	Pro	560	565	570
Ala	Ala	Glu	Glu	Ala	Leu	Asn	Val	Phe	Tyr	Cys	Thr	Tyr	Glu		575	580	585

Gly Ala Val Asp	Leu Asp His Val Thr	Asp Glu Arg Glu Arg Lys	590	595	600
Ala Leu Glu Gly	Ile Ile Ser Asn Phe Gly	Gln Thr Pro Cys Gln	605	610	615
Leu Leu Lys Glu	Pro His Pro Thr Arg	Leu Ser Ala Glu Glu Ala	620	625	630
Ala His Arg Leu	Ala Arg Leu Asp Thr	Asn Ser Pro Ser Ile Phe	635	640	645
Gln His Leu Asp	Glu Leu Lys Ala Phe	Phe Ala Glu Val Thr Val	650	655	660
Ser Ala Ser Gly	Leu Leu Gly Thr His	Ser Trp Leu Pro Tyr Asp	665	670	675
Arg Asn Ile Ser	Asn Tyr Phe Ser Phe	Ser Lys Asp Pro Thr Met	680	685	690
Gly Ser His Lys	Thr Gln Arg Leu Leu	Ser Gly Pro Trp Val Pro	695	700	705
Gly Ser Gly Val	Ser Gly Gln Ala Leu	Ala Val Ala Pro Asp Gly	710	715	720
Lys Leu Leu Phe	Ser Gly Gly His Trp	Asp Gly Ser Leu Arg Val	725	730	735
Thr Ala Leu Pro	Arg Gly Lys Leu Leu	Ser Gln Leu Ser Cys His	740	745	750
Leu Asp Val Val	Thr Cys Leu Ala Leu	Asp Thr Cys Gly Ile Tyr	755	760	765
Leu Ile Ser Gly	Ser Arg Asp Thr Thr	Cys Met Val Trp Arg Leu	770	775	780
Leu His Gln Gly	Gly Leu Ser Val Gly	Leu Ala Pro Lys Pro Val	785	790	795
Gln Val Leu Tyr	Gly His Gly Ala Ala	Val Ser Cys Val Ala Ile	800	805	810
Ser Thr Glu Leu	Asp Met Ala Val Ser	Gly Ser Glu Asp Gly Thr	815	820	825
Val Ile Ile His	Thr Val Arg Arg Gly	Gln Phe Val Ala Ala Leu	830	835	840
Arg Pro Leu Gly	Ala Thr Phe Pro Gly	Pro Ile Phe His Leu Ala	845	850	855
Leu Gly Ser Glu	Gly Gln Ile Val Val	Gln Ser Ser Ala Trp Glu	860	865	870
Arg Pro Gly Ala	Gln Val Thr Tyr Ser	Leu His Leu Tyr Ser Val	875	880	885
Asn Gly Lys Leu	Arg Ala Ser Leu Pro	Leu Ala Glu Gln Pro Thr	890	895	900

Ala Leu Thr Val Thr Glu Asp Phe Val Leu Leu Gly Thr Ala Gln  
905 910

Cys Ala Leu His Ile Leu Gln Leu Asn Thr Leu Leu Pro Ala Ala  
920 925 930

Pro Pro Leu Pro Met Lys Val Ala Ile Arg Ser Val Ala Val Thr  
935 940 945

Lys Glu Arg Ser His Val Leu Val Gly Leu Glu Asp Gly Lys Leu  
950 955 960

Ile Val Val Val Ala Gly Gln Pro Ser Glu Val Arg Ser Ser Gln  
965 970 975

Phe Ala Arg Lys Leu Trp Arg Ser Ser Arg Arg Ile Ser Gln Val  
980 985 990

Ser Ser Gly Glu Thr Glu Tyr Asn Pro Thr Glu Ala Arg  
995 1000

<210> 34

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

tgactgcact acccgtggc aagctgttga gccagctcag ctg 43

<210> 35

<211> 1395

<212> DNA

<213> Homo sapiens

<400> 35

cggacgcgtg ggcggacgcy tgggggctgt gagaaagtc caataaatac 50

atcatgcaac cccacggccc accttgtgaa ctctcgtgc ccagggtga 100

tggtcgctctt ccagggtac tcatccaaag gcctaatacca acgttctgtc 150

ttcaatctgc aaatctatgg ggtcctgggg ctctcttgga ccttaactg 200

ggtactggcc ctgggccaat gcgtcctcgc tggagccttt gectccttct 250

actgggcctt ccacaagccc caggacatcc ctaccttccc cttaatctct 300

gccttcatcc gcacactccg ttaccacact gggtcattgg catttggagc 350

cctcatcctg acccttgtgc agatagcccg ggtcatcttg gagtatattg 400

accacaagct cagaggagtg cagaaccctg tagcccgctg catcatgtgc 450

tgtttcaagt gctgcctctg gtgtctggaa aaatttatca agttcctaaa 500

ccgcaatgca tacatcatga tcgcatcta cggaagaat ttctgtgtct 550

cagccaaaaa tgcgttcatg ctactcatgc gaaacattgt caggggtggc 600

gtctctggaca aagtcaaga cctgctgctg ttctttggga agctgctggt 650

ggctcgaggc gtgggggtcc tgccttctt ttttttctcc ggtcgcatcc 700  
 cggggctggg taaagacttt aagagccccc acctcaacta ttactggctg 750  
 cccatcatga cctccatcct gggggcctat gtcacgcca gcggttctt 800  
 cagcgttttc ggcattgtgt tggacacgct ctctctctgc ttcttggaag 850  
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 agccttctaa agattctggg caagaagaac gaggcgcccc cggacaacaa 950  
 gaagagggaag aagtgcacgc tccggccctg atccaggact gcaccccacc 1000  
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 gaggcaggag aatcgcttga acccgggagg cagaggttgc agtgagccga 1300  
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 aaacaacaaa acaaaaagat ttatttaaag atattttgtt aactc 1395

<210> 36

<211> 321

<212> PRT

<213> Homo sapiens

<400> 36

Arg	Thr	Arg	Gly	Arg	Thr	Arg	Gly	Gly	Cys	Glu	Lys	Val	Pro	Ile	1	5	10	15
Asn	Thr	Ser	Cys	Asn	Pro	Thr	Ala	His	Leu	Val	Asn	Ser	Ser	Cys	20	25	30	
Pro	Gly	Leu	Met	Cys	Val	Phe	Gln	Gly	Tyr	Ser	Ser	Lys	Gly	Leu	35	40	45	
Ile	Gln	Arg	Ser	Val	Phe	Asn	Leu	Gln	Ile	Tyr	Gly	Val	Leu	Gly	50	55	60	
Leu	Phe	Trp	Thr	Leu	Asn	Trp	Val	Leu	Ala	Leu	Gly	Gln	Cys	Val	65	70	75	
Leu	Ala	Gly	Ala	Phe	Ala	Ser	Phe	Tyr	Trp	Ala	Phe	His	Lys	Pro	80	85	90	
Gln	Asp	Ile	Pro	Thr	Phe	Pro	Leu	Ile	Ser	Ala	Phe	Ile	Arg	Thr	95	100	105	
Leu	Arg	Tyr	His	Thr	Gly	Ser	Leu	Ala	Phe	Gly	Ala	Leu	Ile	Leu	110	115	120	
Thr	Leu	Val	Gln	Ile	Ala	Arg	Val	Ile	Leu	Glu	Tyr	Ile	Asp	His	125	130	135	

Lys	Leu	Arg	Gly	Val	Gln	Asn	Pro	Val	Ala	Arg	Cys	Ile	Met	Cys
				140					145					150
Cys	Phe	Lys	Cys	Cys	Leu	Trp	Cys	Leu	Glu	Lys	Phe	Ile	Lys	Phe
				155					160					165
Leu	Asn	Arg	Asn	Ala	Tyr	Ile	Met	Ile	Ala	Ile	Tyr	Gly	Lys	Asn
				170					175					180
Phe	Cys	Val	Ser	Ala	Lys	Asn	Ala	Phe	Met	Leu	Leu	Met	Arg	Asn
				185					190					195
Ile	Val	Arg	Val	Val	Val	Leu	Asp	Lys	Val	Thr	Asp	Leu	Leu	Leu
				200					205					210
Phe	Phe	Gly	Lys	Leu	Leu	Val	Val	Gly	Gly	Val	Gly	Val	Leu	Ser
				215					220					225
Phe	Phe	Phe	Phe	Ser	Gly	Arg	Ile	Pro	Gly	Leu	Gly	Lys	Asp	Phe
				230					235					240
Lys	Ser	Pro	His	Leu	Asn	Tyr	Tyr	Trp	Leu	Pro	Ile	Met	Thr	Ser
				245					250					255
Ile	Leu	Gly	Ala	Tyr	Val	Ile	Ala	Ser	Gly	Phe	Phe	Ser	Val	Phe
				260					265					270
Gly	Met	Cys	Val	Asp	Thr	Leu	Phe	Leu	Cys	Phe	Leu	Glu	Asp	Leu
				275					280					285
Glu	Arg	Asn	Asn	Gly	Ser	Leu	Asp	Arg	Pro	Tyr	Tyr	Met	Ser	Lys
				290					295					300
Ser	Leu	Leu	Lys	Ile	Leu	Gly	Lys	Lys	Asn	Glu	Ala	Pro	Pro	Asp
				305					310					315
Asn	Lys	Lys	Arg	Lys	Lys									
				320										

<210> 37  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 37  
 tcgtgccag gggctgatgt gc 22

<210> 38  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 38  
 gtctttaccc agccccggga tgcg 24

<210> 39  
 <211> 50

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 39  
ggcctaattcc aacgttctgt ctccaatctg caaatctatg gggctcctggg 50

<210> 40  
<211> 1365  
<212> DNA  
<213> Homo sapiens

<400> 40  
gagtccttgac cgcgcgcggg ctcttggtac ctcagcgoga gcgccaggcg 50  
tccggccgcc gtggctatgt tcgtgtccga ttccgcgcaa gagttctacg 100  
agggtgtcca gagccagagg gtccctctct tcgtggcctc ggacgtggat 150  
gctctgtgtg cgtgcaagat ccttcaggcc ttgttcacgt gtgaccacgt 200  
gcaatatacg ctggttccag ttctgggtg gcaagaactt gaaactgcat 250  
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gacatcgtca gccatggtga tgtttgagct ggcttggatg ctgtccaagg 700  
acctgaatga catgctgtgt tggggcatcg ttggactaac agaccagtgg 750  
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gcagcgccac gtttccgcc acaaccaccg gaacgaggat gaggagaaca 850  
cactctccgt ggactgcaca cggatctcct ttgagtatga cctccgctg 900  
gtgctctacc agcaactggt cctccatgac agcctgtgca acaccagcta 950  
taccgcagcc aggttcaagc tgtggtctgt gcatggacag aagcggtccc 1000  
aggagtctct tgcagacatg ggtcttcccc tgaagcaggt gaagcagaag 1050  
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gcattcattt tgggttcaag cacaagtttc tggccagcga cgtggtcttt 1200



gccaccatgt ctttgatgga gagccccgag aaggatggct cagggacaga 1250  
 tcacttcac caggctctgg acagcctctc caggagtaac ctggacaagc 1300  
 tgtaccatgg cctggaactc gccaaagaagc agctgcgagc caccagcag 1350  
 accattgcc a gctgc 1365

<210> 41  
 <211> 566  
 <212> PRT  
 <213> Homo sapiens

<400> 41  
 Met Phe Val Ser Asp Phe Arg Lys Glu Phe Tyr Glu Val Val Gln  
 1 5 10 15  
 Ser Gln Arg Val Leu Phe Val Ala Ser Asp Val Asp Ala Leu  
 20 25 30  
 Cys Ala Cys Lys Ile Leu Gln Ala Leu Phe Gln Cys Asp His Val  
 35 40 45  
 Gln Tyr Thr Leu Val Pro Val Ser Gly Trp Gln Glu Leu Glu Thr  
 50 55 60  
 Ala Phe Leu Glu His Lys Glu Gln Phe His Tyr Phe Ile Leu Ile  
 65 70 75  
 Asn Cys Gly Ala Asn Val Asp Leu Leu Asp Ile Leu Gln Pro Asp  
 80 85 90  
 Glu Asp Thr Ile Phe Val Cys Asp Ser His Arg Pro Val Asn  
 95 100 105  
 Val Val Asn Val Tyr Asn Asp Thr Gln Ile Lys Leu Leu Ile Lys  
 110 115 120  
 Gln Asp Asp Asp Leu Glu Val Pro Ala Tyr Glu Asp Ile Phe Arg  
 125 130 135  
 Asp Glu Glu Glu Asp Glu Glu His Ser Gly Asn Asp Ser Asp Gly  
 140 145 150  
 Ser Glu Pro Ser Glu Lys Arg Thr Arg Leu Glu Glu Glu Ile Val  
 155 160 165  
 Glu Gln Thr Met Arg Arg Arg Gln Arg Arg Glu Trp Glu Ala Arg  
 170 175 180  
 Arg Arg Asp Ile Leu Phe Asp Tyr Glu Gln Tyr Glu Tyr His Gly  
 185 190 195  
 Thr Ser Ser Ala Met Val Met Phe Glu Leu Ala Trp Met Leu Ser  
 200 205 210  
 Lys Asp Leu Asn Asp Met Leu Trp Trp Ala Ile Val Gly Leu Thr  
 215 220 225  
 Asp Gln Trp Val Gln Asp Lys Ile Thr Gln Met Lys Tyr Val Thr  
 230 235 240  
 Asp Val Gly Val Leu Gln Arg His Val Ser Arg His Asn His Arg

	245		250		255
Asn Glu Asp Glu	Glu Asn Thr Leu Ser	Val Asp Cys Thr Arg	Ile		
	260		265		270
Ser Phe Glu Tyr	Asp Leu Arg Leu Val	Leu Tyr Gln His Trp	Ser		
	275		280		285
Leu His Asp Ser	Leu Cys Asn Thr Ser	Tyr Thr Ala Ala Arg	Phe		
	290		295		300
Lys Leu Trp Ser	Val His Gly Gln Lys	Arg Leu Gln Glu Phe	Leu		
	305		310		315
Ala Asp Met Gly	Leu Pro Leu Lys Gln	Val Lys Gln Lys Phe	Gln		
	320		325		330
Ala Met Asp Ile	Ser Leu Lys Glu Asn	Leu Arg Glu Met Ile	Glu		
	335		340		345
Glu Ser Ala Asn	Lys Phe Gly Met Lys	Asp Met Arg Val Gln	Thr		
	350		355		360
Phe Ser Ile His	Phe Gly Phe Lys His	Lys Phe Leu Ala Ser	Asp		
	365		370		375
Val Val Phe Ala	Thr Met Ser Leu Met	Glu Ser Pro Glu Lys	Asp		
	380		385		390
Gly Ser Gly Thr	Asp His Phe Ile Gln	Ala Leu Asp Ser Leu	Ser		
	395		400		405
Arg Ser Asn Leu	Asp Lys Leu Tyr His	Gly Leu Glu Leu Ala	Lys		
	410		415		420
Lys Gln Leu Arg	Ala Thr Gln Gln Thr	Ile Ala Ser Cys Leu	Cys		
	425		430		435
Thr Asn Leu Val	Ile Ser Gln Gly Pro	Phe Leu Tyr Cys Ser	Leu		
	440		445		450
Met Glu Gly Thr	Pro Asp Val Met Leu	Phe Ser Arg Pro Ala	Ser		
	455		460		465
Leu Ser Leu Leu	Ser Lys His Leu Leu	Lys Ser Phe Val Cys	Ser		
	470		475		480
Thr Lys Asn Arg	Arg Cys Lys Leu Leu	Pro Leu Val Met Ala	Ala		
	485		490		495
Pro Leu Ser Met	Glu His Gly Thr Val	Thr Val Val Gly Ile	Pro		
	500		505		510
Pro Glu Thr Asp	Ser Ser Asp Arg Lys	Asn Phe Phe Gly Arg	Ala		
	515		520		525
Phe Glu Lys Ala	Ala Glu Ser Thr Ser	Ser Arg Met Leu His	Asn		
	530		535		540
His Phe Asp Leu	Ser Val Ile Glu Leu	Lys Ala Glu Asp Arg	Ser		
	545		550		555
Lys Phe Leu Asp	Ala Leu Ile Ser Leu	Leu Ser			

<210> 42  
 <211> 380  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 44, 118, 172, 183  
 <223> unknown base

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 ctcttcgtgg cctcggangt ggatgctctg tgtgcgtgca agatccttca 150  
 ggcccttggt cagtgtgacc angtgcaata tangctggtt ccagtttctg 200  
 ggtggcaaga acttgaaact gcatttcttg agcataaaga acagtttcat 250  
 tatttttatto tcataaactg tggagctaata gtagacctat tggatattct 300  
 tcaacctgat gaagacacta tattctttgt gtgtgacacc cataggccag 350  
 tcaatgttgt caatgtatac aacgataccc 380

<210> 43  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 43  
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<210> 44  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 44  
 attgacaaca ttgactggcc tatggg 26

<210> 45  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 45  
 gtggatgctc tgtgtgcgtg caagatcctt caggccttgt tccagtgtga 50

<210> 46

<211> 3089  
 <212> DNA  
 <213> Homo sapiens

<400> 46  
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 ttcttagtga accacgaagg gacgatacca gaaaacaccc toaacccaaa 100  
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 aggaacgaaa agagacagtt ttttttgaa agctaagtct tccctttatc 200  
 gagtcaagaa accccccctt ctgagctat ttacagcttt taacaattga 250  
 gtaaagtacg ctccggtcac catggtgaca gccgccctgg gtcctgtctg 300  
 ggagcgcctc ctgctctttc tctgatgtg tgagatccgt atggtggagc 350  
 tcacctttga cagagctgtg gccagcggct gccaacgggt ctgtgactct 400  
 gaggaacccc tggatctctg ccattgtatc tcagcctctt cctccggccg 450  
 ccccacgcc ctgcctgaga tcagacccta cattaatatc accatcttga 500  
 aggggtgcaa aggggaccca ggccaatgg gcctgccagg gtacatgggc 550  
 agggagggtc cccaagggga gcctggcctc cagggcagca aggggtgcaa 600  
 gggggagatg ggcagccccg gcgccccgtg ccagaagcgc ttcttcgcct 650  
 tctcagtggg ccgcaagacg gcctgcaca ggcgcgagga ctccagacg 700  
 ctgctcttcg aaagggtctt tgtgaacctt gatgggtgct ttgacatggc 750  
 gaccggccag tttgctgctc ccctgcgtgg catctacttc ttcagcctca 800  
 atgtgcacag ctggaattac aaggagacgt acgtgcacat tatgcataac 850  
 cagaaaaggg ctgtcatcct gtacgcgcag cccagcgcgc gcagcatcat 900  
 gcagagccag agtgtgatgc tggacctggc ctacggggac cgcgtctggg 950  
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 ccagcaactc toaaacttgg aaatgcatgc gaatcaccgc gggttcgtgt 1350  
 taaatgcaga ttctgactca gcaggtctga gtgggtocag gattctgtgt 1400  
 ttctcatatg ttctgggtg atgctgatgg gtcagctcta tgaaccacac 1450

tggagcaacc aggtttctagg actttctcaa tattctagta ctttctgaac 1500  
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 tcattcatta aacactgagc actcactctg tgcctgggtcc cggaagggt 2000  
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taaagaatgc tgtctcctct tggaaaaaaa aaaaaaaaaa 3089

<210> 47

<211> 259

<212> PRT

<213> Homo sapiens

<220>

<221> Signal Peptide

<222> 1-20

<223> Signal Peptide

<220>

<221> N-glycosylation Site

<222> 72-75

<223> N-glycosylation Site

<220>

<221> Clq Domain Proteins

<222> 144-178, 78-111, 84-117

<223> Clq Domain Proteins

<400> 47

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Phe	Leu	Leu	Met	Cys	Glu	Ile	Arg	Met	Val	Glu	Leu	Thr	Phe	Asp
				20					25					30
Arg	Ala	Val	Ala	Ser	Gly	Cys	Gln	Arg	Cys	Cys	Asp	Ser	Glu	Asp
				35					40					45
Pro	Leu	Asp	Pro	Ala	His	Val	Ser	Ser	Ala	Ser	Ser	Ser	Gly	Arg
				50					55					60
Pro	His	Ala	Leu	Pro	Glu	Ile	Arg	Pro	Tyr	Ile	Asn	Ile	Thr	Ile
				65					70					75
Leu	Lys	Gly	Asp	Lys	Gly	Asp	Pro	Gly	Pro	Met	Gly	Leu	Pro	Gly
				80					85					90
Tyr	Met	Gly	Arg	Glu	Gly	Pro	Gln	Gly	Glu	Pro	Gly	Pro	Gln	Gly
				95					100					105
Ser	Lys	Gly	Asp	Lys	Gly	Glu	Met	Gly	Ser	Pro	Gly	Ala	Pro	Cys
				110					115					120
Gln	Lys	Arg	Phe	Phe	Ala	Phe	Ser	Val	Gly	Arg	Lys	Thr	Ala	Leu
				125					130					135
His	Ser	Gly	Glu	Asp	Phe	Gln	Thr	Leu	Leu	Phe	Glu	Arg	Val	Phe
				140					145					150
Val	Asn	Leu	Asp	Gly	Cys	Phe	Asp	Met	Ala	Thr	Gly	Gln	Phe	Ala
				155					160					165
Ala	Pro	Leu	Arg	Gly	Ile	Tyr	Phe	Phe	Ser	Leu	Asn	Val	His	Ser
				170					175					180
Trp	Asn	Tyr	Lys	Glu	Thr	Tyr	Val	His	Ile	Met	His	Asn	Gln	Lys
				185					190					195
Glu	Ala	Val	Ile	Leu	Tyr	Ala	Gln	Pro	Ser	Glu	Arg	Ser	Ile	Met

	200		205		210
Gln Ser Gln Ser	Val Met Leu Asp Leu	Ala Tyr Gly Asp Arg	Val		
	215	220			
Trp Val Arg Leu	Phe Lys Arg Gln Arg	Glu Asn Ala Ile Tyr	Ser		
	230	235	240		
Asn Asp Phe Asp	Thr Tyr Ile Thr Phe	Ser Gly His Leu Ile	Lys		
	245	250	255		
Ala Glu Asp Asp					

<210> 48  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 48  
 ccagacgctg ctcttcgaaa gggtc 25

<210> 49  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 49  
 ggtcccgta ggccaggtec agc 23

<210> 50  
 <211> 50  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 50  
 ctacttcttc agcctcaatg tgcacagctg gaattacaag gagacgtacg 50

<210> 51  
 <211> 2768  
 <212> DNA  
 <213> Homo sapiens

<400> 51  
 actcgaacgc agttgcttcg ggacccagga cccctcggg cccgaccgc 50  
 caggaaagac tgaggccgag gcctgccccg ccgggtccc tgcgccgag 100  
 ccgcctcccg ggacagaaga tgtgctccag ggtccctctg ctgctgccg 150  
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 ttcccatatt attctgggaa gatgttttc aaactcagag acaaggactt 2700  
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 aaaagatgaa gtgtgaaa 2768

<210> 52  
 <211> 673  
 <212> PRT  
 <213> Homo sapiens

<400> 52  
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 Ala Leu Gly Pro Gly Val Gln Gly Cys Pro Ser Gly Cys Gln Cys 30  
 20 25 30  
 Ser Gln Pro Gln Thr Val Phe Cys Thr Ala Arg Gln Gly Thr Thr 45  
 35 40 45  
 Val Pro Arg Asp Val Pro Pro Asp Thr Val Gly Leu Tyr Val Phe 60  
 50 55 60  
 Glu Asn Gly Ile Thr Met Leu Asp Ala Gly Ser Phe Ala Gly Leu 75  
 65 70 75  
 Pro Gly Leu Gln Leu Leu Asp Leu Ser Gln Asn Gln Ile Ala Ser 90  
 80 85 90  
 Leu Pro Ser Gly Val Phe Gln Pro Leu Ala Asn Leu Ser Asn Leu

95					100					105						
Asp	Leu	Thr	Ala	110	Asn	Arg	Leu	His	Glu	Ile	Thr	Asn	Glu	Thr	Phe	120
Arg	Gly	Leu	Arg	125	Arg	Leu	Glu	Arg	Leu	Tyr	Leu	Gly	Lys	Asn	Arg	135
Ile	Arg	His	Ile	140	Gln	Pro	Gly	Ala	Phe	Asp	Thr	Leu	Asp	Arg	Leu	150
Leu	Glu	Leu	Lys	155	Leu	Gln	Asp	Asn	Glu	Leu	Arg	Ala	Leu	Pro	Pro	165
Leu	Arg	Leu	Pro	170	Arg	Leu	Leu	Leu	Leu	Asp	Leu	Ser	His	Asn	Ser	180
Leu	Leu	Ala	Leu	185	Glu	Pro	Gly	Ile	Leu	Asp	Thr	Ala	Asn	Val	Glu	195
Ala	Leu	Arg	Leu	200	Ala	Gly	Leu	Gly	Leu	Gln	Gln	Leu	Asp	Glu	Gly	210
Leu	Phe	Ser	Arg	215	Leu	Arg	Asn	Leu	His	Asp	Leu	Asp	Val	Ser	Asp	225
Asn	Gln	Leu	Glu	230	Arg	Val	Pro	Pro	Val	Ile	Arg	Gly	Leu	Arg	Gly	240
Leu	Thr	Arg	Leu	245	Arg	Leu	Ala	Gly	Asn	Thr	Arg	Ile	Ala	Gln	Leu	255
Arg	Pro	Glu	Asp	260	Leu	Ala	Gly	Leu	Ala	Ala	Leu	Gln	Glu	Leu	Asp	270
Val	Ser	Asn	Leu	275	Ser	Leu	Gln	Ala	Leu	Pro	Gly	Asp	Leu	Ser	Gly	285
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Asn	Cys	Val	Cys	305	Pro	Leu	Ser	Trp	Phe	Gly	Pro	Trp	Val	Arg	Glu	315
Ser	His	Val	Thr	320	Leu	Ala	Ser	Pro	Glu	Glu	Thr	Arg	Cys	His	Phe	330
Pro	Pro	Lys	Asn	335	Ala	Gly	Arg	Leu	Leu	Leu	Glu	Leu	Asp	Tyr	Ala	345
Asp	Phe	Gly	Cys	350	Pro	Ala	Thr	Thr	Thr	Thr	Ala	Thr	Val	Pro	Thr	360
Thr	Arg	Pro	Val	365	Val	Arg	Glu	Pro	Thr	Ala	Leu	Ser	Ser	Ser	Leu	375
Ala	Pro	Thr	Trp	380	Leu	Ser	Pro	Thr	Ala	Pro	Ala	Thr	Glu	Ala	Pro	390
Ser	Pro	Pro	Ser	395	Thr	Ala	Pro	Pro	Thr	Val	Gly	Pro	Val	Pro	Gln	405
Pro	Gln	Asp	Cys		Pro	Pro	Ser	Thr	Cys	Leu	Asn	Gly	Gly	Thr	Cys	

	410		415		420
His Leu Gly Thr	Arg His His Leu Ala Cys	Leu Cys Pro Glu Gly			
	425		430		435
Phe Thr Gly Leu	Tyr Cys Glu Ser Gln Met	Gly Gln Gly Thr Arg			
	440		445		450
Pro Ser Pro Thr	Pro Val Thr Pro Arg Pro	Pro Arg Ser Leu Thr			
	455		460		465
Leu Gly Ile Glu	Pro Val Ser Pro Thr Ser	Leu Arg Val Gly Leu			
	470		475		480
Gln Arg Tyr Leu	Gln Gly Ser Ser Val Gln	Leu Arg Ser Leu Arg			
	485		490		495
Leu Thr Tyr Arg	Asn Leu Ser Gly Pro Asp	Lys Arg Leu Val Thr			
	500		505		510
Leu Arg Leu Pro	Ala Ser Leu Ala Glu Tyr	Thr Val Thr Gln Leu			
	515		520		525
Arg Pro Asn Ala	Thr Tyr Ser Val Cys Val	Met Pro Leu Gly Pro			
	530		535		540
Gly Arg Val Pro	Glu Gly Glu Glu Ala Cys	Gly Glu Ala His Thr			
	545		550		555
Pro Pro Ala Val	His Ser Asn His Ala Pro	Val Thr Gln Ala Arg			
	560		565		570
Glu Gly Asn Leu	Pro Leu Leu Ile Ala Pro	Ala Leu Ala Ala Val			
	575		580		585
Leu Leu Ala Ala	Leu Ala Ala Val Gly Ala	Ala Tyr Cys Val Arg			
	590		595		600
Arg Gly Arg Ala	Met Ala Ala Ala Ala Gln	Asp Lys Gly Gln Val			
	605		610		615
Gly Pro Gly Ala	Gly Pro Leu Glu Leu Glu	Gly Val Lys Val Pro			
	620		625		630
Leu Glu Pro Gly	Pro Lys Ala Thr Glu Gly	Gly Gly Glu Ala Leu			
	635		640		645
Pro Ser Gly Ser	Glu Cys Glu Val Pro Leu	Met Gly Phe Pro Gly			
	650		655		660
Pro Gly Leu Gln	Ser Pro Leu His Ala Lys	Pro Tyr Ile			
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<210> 53

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 53

tcttcagccg cttgcgcaac ctc 23

<210> 54  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 54  
ttgtccacat ccagctcctg cagg 24

<210> 55  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 55  
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<210> 56  
<211> 3462  
<212> DNA  
<213> Homo sapiens

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ttatgacagc agagggtgat gctccagagc tgccagaaga aagggaactg 200  
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cccagccaca acgacactgg atttatccta taacctcctt tttcaactoc 300  
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cataacagaa ttcaacagct ggatctcaaa acctttgaat tcaacaagga 400  
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gaagaaggta gcctgcccac cttaaacaca acaaaactgc acattgtttt 700  
accaatggac acaaatcttc ggggtctttt gcgtgatgga atcaagactt 750  
caaaaatatt agaaatgaca aatataatag gcaaaagcca atttgaagt 800  
tatgaaatgc aacgaaatct tagtttagaa aatgctaaga catcggttct 850  
attgcttaat aaagttgatt taactctgga cgaccttttc cttatcttac 900

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tgtaatgaga actataaaat tggagcatgt acatttcaga gtgttttaca 1050  
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ctgacaatat caaatgcaca aatgccacac atgcttttcc cgaattatcc 1150  
tacgaaattc caatatttaa attttgccaa taatatctta acagacgagt 1200  
tgtttaaaag aactatccaa ctgcctcact tgaaaactct cattttgaat 1250  
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 gatacaacct ttatgatggc aatttgacaa tatttattaa aataaaaaat 2650  
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 ggtatggaaa aaacatatata atagtgtata aactattagg ttggtgcaaa 3250  
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 acaggggagca tttgatttct atgttggtgta ttctataat gtttgaattg 3400  
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<210> 57  
 <211> 811  
 <212> PRT  
 <213> Homo sapiens

<400> 57  
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 20 25 30  
 Met Thr Asn Cys Ser Asn Met Ser Leu Arg Lys Val Pro Ala Asp  
 35 40 45  
 Leu Thr Pro Ala Thr Thr Thr Leu Asp Leu Ser Tyr Asn Leu Leu  
 50 55 60  
 Phe Gln Leu Gln Ser Ser Asp Phe His Ser Val Ser Lys Leu Arg  
 65 70 75  
 Val Leu Ile Leu Cys His Asn Arg Ile Gln Gln Leu Asp Leu Lys  
 80 85 90

Thr	Phe	Glu	Phe	Asn	Lys	Glu	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	Asn	
				95					100					105	
Asn	Arg	Leu	Lys	Ser	Val	Thr	Trp	Tyr	Leu	Leu	Ala	Gly	Leu	Arg	
				110					115					120	
Tyr	Leu	Asp	Leu	Ser	Phe	Asn	Asp	Phe	Asp	Thr	Met	Pro	Ile	Cys	
				125					130					135	
Glu	Glu	Ala	Gly	Asn	Met	Ser	His	Leu	Glu	Ile	Leu	Gly	Leu	Ser	
				140					145					150	
Gly	Ala	Lys	Ile	Gln	Lys	Ser	Asp	Phe	Gln	Lys	Ile	Ala	His	Leu	
				155					160					165	
His	Leu	Asn	Thr	Val	Phe	Leu	Gly	Phe	Arg	Thr	Leu	Pro	His	Tyr	
				170					175					180	
Glu	Glu	Gly	Ser	Leu	Pro	Ile	Leu	Asn	Thr	Thr	Lys	Leu	His	Ile	
				185					190					195	
Val	Leu	Pro	Met	Asp	Thr	Asn	Phe	Trp	Val	Leu	Leu	Arg	Asp	Gly	
				200					205					210	
Ile	Lys	Thr	Ser	Lys	Ile	Leu	Glu	Met	Thr	Asn	Ile	Asp	Gly	Lys	
				215					220					225	
Ser	Gln	Phe	Val	Ser	Tyr	Glu	Met	Gln	Arg	Asn	Leu	Ser	Leu	Glu	
				230					235					240	
Asn	Ala	Lys	Thr	Ser	Val	Leu	Leu	Leu	Asn	Lys	Val	Asp	Leu	Leu	
				245					250					255	
Trp	Asp	Asp	Leu	Phe	Leu	Ile	Leu	Gln	Phe	Val	Trp	His	Thr	Ser	
				260					265					270	
Val	Glu	His	Phe	Gln	Ile	Arg	Asn	Val	Thr	Phe	Gly	Gly	Lys	Ala	
				275					280					285	
Tyr	Leu	Asp	His	Asn	Ser	Phe	Asp	Tyr	Ser	Asn	Thr	Val	Met	Arg	
				290					295					300	
Thr	Ile	Lys	Leu	Glu	His	Val	His	Phe	Arg	Val	Phe	Tyr	Ile	Gln	
				305					310					315	
Gln	Asp	Lys	Ile	Tyr	Leu	Leu	Leu	Thr	Lys	Met	Asp	Ile	Glu	Asn	
				320					325					330	
Leu	Thr	Ile	Ser	Asn	Ala	Gln	Met	Pro	His	Met	Leu	Phe	Pro	Asn	
				335					340					345	
Tyr	Pro	Thr	Lys	Phe	Gln	Tyr	Leu	Asn	Phe	Ala	Asn	Asn	Ile	Leu	
				350					355					360	
Thr	Asp	Glu	Leu	Phe	Lys	Arg	Thr	Ile	Gln	Leu	Pro	His	Leu	Lys	
				365					370					375	
Thr	Leu	Ile	Leu	Asn	Gly	Asn	Lys	Leu	Glu	Thr	Leu	Ser	Leu	Val	
				380					385					390	
Ser	Cys	Phe	Ala	Asn	Asn	Thr	Pro	Leu	Glu	His	Leu	Asp	Leu	Ser	
				395					400					405	

Gln Asn Leu Leu	Gln His Lys Asn Asp	Glu Asn Cys Ser Trp	Pro
410		415	420
Glu Thr Val Val	Asn Met Asn Leu Ser	Tyr Asn Lys Leu Ser	Asp
425		430	435
Ser Val Phe Arg	Cys Leu Pro Lys Ser	Ile Gln Ile Leu Asp	Leu
440		445	450
Asn Asn Asn Gln	Ile Gln Thr Val Pro	Lys Glu Thr Ile His	Leu
455		460	465
Met Ala Leu Arg	Glu Leu Asn Ile Ala	Phe Asn Phe Leu Thr	Asp
470		475	480
Leu Pro Gly Cys	Ser His Phe Ser Arg	Leu Ser Val Leu Asn	Ile
485		490	495
Glu Met Asn Phe	Ile Leu Ser Pro Ser	Leu Asp Phe Val Gln	Ser
500		505	510
Cys Gln Glu Val	Lys Thr Leu Asn Ala	Gly Arg Asn Pro Phe	Arg
515		520	525
Cys Thr Cys Glu	Leu Lys Asn Phe Ile	Gln Leu Glu Thr Tyr	Ser
530		535	540
Glu Val Met Met	Val Gly Trp Ser Asp	Ser Tyr Thr Cys Glu	Tyr
545		550	555
Pro Leu Asn Leu	Arg Gly Thr Arg Leu	Lys Asp Val His Leu	His
560		565	570
Glu Leu Ser Cys	Asn Thr Ala Leu Leu	Ile Val Thr Ile Val	Val
575		580	585
Ile Met Leu Val	Leu Gly Leu Ala Val	Ala Phe Cys Cys Leu	His
590		595	600
Phe Asp Leu Pro	Trp Tyr Leu Arg Met	Leu Gly Gln Cys Thr	Gln
605		610	615
Thr Trp His Arg	Val Arg Lys Thr Thr	Gln Glu Gln Leu Lys	Arg
620		625	630
Asn Val Arg Phe	His Ala Phe Ile Ser	Tyr Ser Glu His Asp	Ser
635		640	645
Leu Trp Val Lys	Asn Glu Leu Ile Pro	Asn Leu Glu Lys Glu	Asp
650		655	660
Gly Ser Ile Leu	Ile Cys Leu Tyr Glu	Ser Tyr Phe Asp Pro	Gly
665		670	675
Lys Ser Ile Ser	Glu Asn Ile Val Ser	Phe Ile Glu Lys Ser	Tyr
680		685	690
Lys Ser Ile Phe	Val Leu Ser Pro Asn	Phe Val Gln Asn Glu	Trp
695		700	705
Cys His Tyr Glu	Phe Tyr Phe Ala His	His Asn Leu Phe His	Glu
710		715	720



Asn	Ser	Asp	His	Ile	Ile	Leu	Ile	Leu	Leu	Glu	Pro	Ile	Pro	Phe
				725						730				735
Tyr	Cys	Ile	Pro	Thr	Arg	Tyr	His	Lys	Leu	Lys	Ala	Leu	Leu	Glu
				740					745					750
Lys	Lys	Ala	Tyr	Leu	Glu	Trp	Pro	Lys	Asp	Arg	Arg	Lys	Cys	Gly
				755					760					765
Leu	Phe	Trp	Ala	Asn	Leu	Arg	Ala	Ala	Ile	Asn	Val	Asn	Val	Leu
				770					775					780
Ala	Thr	Arg	Glu	Met	Tyr	Glu	Leu	Gln	Thr	Phe	Thr	Glu	Leu	Asn
				785					790					795
Glu	Glu	Ser	Arg	Gly	Ser	Thr	Ile	Ser	Leu	Met	Arg	Thr	Asp	Cys
				800					805					810

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<210> 58  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 58  
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<210> 59  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 59  
 ttatagacaa tctgtttctca tcagaga 27

<210> 60  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 60  
 aaaaagcata cttggaatgg cccaaggata ggtgtaaatg 40

<210> 61  
 <211> 3772  
 <212> DNA  
 <213> Homo sapiens

<400> 61  
 gggggctttc ttgggcttgg ctgcttgga cactgcctc caaggaccg 50  
 cctcgagggg gtcgccggga aaggaggga agaaggaagg gcggggccgg 100



taaacacgct gctctgggag gcagaggatc gacagaatgt ccccaggaaa 1750  
 gtcccacatc actatatatgc aatccctgag tggtttctgt cggaatatgc 1800  
 caccgttggtc gccgagacca gagcagtcac agcctggatg gaaaaaatcc 1850  
 cttttgtgct gggcggaac ctgcagggcg gcgagctggt ggtggcgat 1900  
 ccctacgaac tggcgcggtc cccctggaag acgcaggaaac acacccccac 1950  
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 cttttgttta atgttgctgc ctcattgacc tgggaaaaat gaaaaaaaaa 3700  
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 aaaaaaaaaa aaaaaaaaaa aa 3772

<210> 62  
 <211> 756  
 <212> PRT  
 <213> Homo sapiens

<400> 62  
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 20 25 30  
 Glu Asp Pro Asp Tyr Tyr Gly Gln Glu Ile Trp Ser Arg Glu Pro  
 35 40 45  
 Tyr Tyr Ala Arg Pro Glu Pro Glu Leu Glu Thr Phe Ser Pro Pro  
 50 55 60  
 Leu Pro Ala Gly Pro Gly Glu Glu Trp Glu Arg Arg Pro Gln Glu  
 65 70 75  
 Pro Arg Pro Pro Lys Arg Ala Thr Lys Pro Lys Lys Ala Pro Lys  
 80 85 90  
 Arg Glu Lys Ser Ala Pro Glu Pro Pro Pro Gly Lys His Ser  
 95 100 105  
 Asn Lys Lys Val Met Arg Thr Lys Ser Ser Glu Lys Ala Ala Asn  
 110 115 120  
 Asp Asp His Ser Val Arg Val Ala Arg Glu Asp Val Arg Glu Ser  
 125 130 135  
 Cys Pro Pro Leu Gly Leu Glu Thr Leu Lys Ile Thr Asp Phe Gln  
 140 145 150  
 Leu His Ala Ser Thr Val Lys Arg Tyr Gly Leu Gly Ala His Arg  
 155 160 165  
 Gly Arg Leu Asn Ile Gln Ala Gly Ile Asn Glu Asn Asp Phe Tyr  
 170 175 180  
 Asp Gly Ala Trp Cys Ala Gly Arg Asn Asp Leu Gln Gln Trp Ile

	185		190		195
Glu Val Asp Ala	Arg Arg Leu Thr Arg Phe	Thr Gly Val Ile Thr			
	200		205		210
Gln Gly Arg Asn	Ser Leu Trp Leu Ser Asp	Trp Val Thr Ser Tyr			
	215		220		225
Lys Val Met Val	Ser Asn Asp Ser His Thr	Trp Val Thr Val Lys			
	230		235		240
Asn Gly Ser Gly	Asp Met Ile Phe Glu Gly	Asn Ser Glu Lys Glu			
	245		250		255
Ile Pro Val Leu	Asn Glu Leu Pro Val Pro	Met Val Ala Arg Tyr			
	260		265		270
Ile Arg Ile Asn	Pro Gln Ser Trp Phe Asp	Asn Gly Ser Ile Cys			
	275		280		285
Met Arg Met Glu	Ile Leu Gly Cys Pro Leu	Pro Asp Pro Asn Asn			
	290		295		300
Tyr Tyr His Arg	Arg Asn Glu Met Thr Thr	Thr Asp Asp Leu Asp			
	305		310		315
Phe Lys His His	Asn Tyr Lys Glu Met Arg	Gln Leu Met Lys Val			
	320		325		330
Val Asn Glu Met	Cys Pro Asn Ile Thr Arg	Ile Tyr Asn Ile Gly			
	335		340		345
Lys Ser His Gln	Gly Leu Lys Leu Tyr Ala	Val Glu Ile Ser Asp			
	350		355		360
His Pro Gly Glu	His Glu Val Gly Glu Pro	Glu Phe His Tyr Ile			
	365		370		375
Ala Gly Ala His	Gly Asn Glu Val Leu Gly	Arg Glu Leu Leu Leu			
	380		385		390
Leu Leu Val Gln	Phe Val Cys Gln Glu Tyr	Leu Ala Arg Asn Ala			
	395		400		405
Arg Ile Val His	Leu Val Glu Glu Thr Arg	Ile His Val Leu Pro			
	410		415		420
Ser Leu Asn Pro	Asp Gly Tyr Glu Lys Ala	Tyr Glu Gly Gly Ser			
	425		430		435
Glu Leu Gly Gly	Trp Ser Leu Gly Arg Trp	Thr His Asp Gly Ile			
	440		445		450
Asp Ile Asn Asn	Asn Phe Pro Asp Leu Asn	Thr Leu Leu Trp Glu			
	455		460		465
Ala Glu Asp Arg	Gln Asn Val Pro Arg Lys	Val Pro Asn His Tyr			
	470		475		480
Ile Ala Ile Pro	Glu Trp Phe Leu Ser Glu	Asn Ala Thr Val Ala			
	485		490		495
Ala Glu Thr Arg	Ala Val Ile Ala Trp Met	Glu Lys Ile Pro Phe			

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Val Leu Gly Gly Asn Leu Gln Gly Gly Glu Leu Val Val Ala Tyr		
515	520	525
Pro Tyr Asp Leu Val Arg Ser Pro Trp Lys Thr Gln Glu His Thr		
530	535	540
Pro Thr Pro Asp Asp His Val Phe Arg Trp Leu Ala Tyr Ser Tyr		
545	550	555
Ala Ser Thr His Arg Leu Met Thr Asp Ala Arg Arg Arg Val Cys		
560	565	570
His Thr Glu Asp Phe Gln Lys Glu Glu Gly Thr Val Asn Gly Ala		
575	580	585
Ser Trp His Thr Val Ala Gly Ser Leu Asn Asp Phe Ser Tyr Leu		
590	595	600
His Thr Asn Cys Phe Glu Leu Ser Ile Tyr Val Gly Cys Asp Lys		
605	610	615
Tyr Pro His Glu Ser Gln Leu Pro Glu Glu Trp Glu Asn Asn Arg		
620	625	630
Glu Ser Leu Ile Val Phe Met Glu Gln Val His Arg Gly Ile Lys		
635	640	645
Gly Leu Val Arg Asp Ser His Gly Lys Gly Ile Pro Asn Ala Ile		
650	655	660
Ile Ser Val Glu Gly Ile Asn His Asp Ile Arg Thr Ala Asn Asp		
665	670	675
Gly Asp Tyr Trp Arg Leu Leu Asn Pro Gly Glu Tyr Val Val Thr		
680	685	690
Ala Lys Ala Glu Gly Phe Thr Ala Ser Thr Lys Asn Cys Met Val		
695	700	705
Gly Tyr Asp Met Gly Ala Thr Arg Cys Asp Phe Thr Leu Ser Lys		
710	715	720
Thr Asn Met Ala Arg Ile Arg Glu Ile Met Glu Lys Phe Gly Lys		
725	730	735
Gln Pro Val Ser Leu Pro Ala Arg Arg Leu Lys Leu Arg Gly Arg		
740	745	750
Lys Arg Arg Gln Arg Gly		
755		

<210> 63

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 63

gttctcaatg agctaccgt cccc 24

<210> 64  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 64  
 cgcgatgtag tggaactcgg gctc 24

<210> 65  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 65  
 atccgcataa accctcagtc ctggtttgat aatgggagca totgcatgag 50

<210> 66  
 <211> 2854  
 <212> DNA  
 <213> Homo sapiens

<400> 66  
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 tcttcottgg ccaagctgoa ggggatttgg gggatgtggg acctccaatt 100  
 cccagcccg gcttcagctc tttcccaggt gttgactcca gctccagctt 150  
 cagctccagc tccaggtcgg gctccagctc cagccgcagc ttaggcagcg 200  
 gaggttctgt gtcccagttg ttttccaatt tcaccggctc cgtggatgac 250  
 cgtgggacct gccagtgctc tgtttcctg ccagacacca cettccctg 300  
 ggacagagtg gaacgcttgg aattcacagc tcatgttctt tctcagaagt 350  
 ttgagaaaaga actttctaaa gtgaggggaat atgtccaatt aattagtgtg 400  
 tatgaaaaga aactgttaaa cctaactgtc cgaattgaca tcattggagaa 450  
 ggataccatt tcttacactg aactggactt cgagctgac aaggtagaag 500  
 tgaaggagat ggaaaaactg gtcatacagc tgaaggagag ttttggtgga 550  
 agctcagaaa ttgttgacca gctggaggtg gagataagaa atatgactct 600  
 cttggtgag aagcttgaga cactagacaa aaacaatgtc cttgccattc 650  
 gccgagaaat cgtggctctg aagaccaagc tgaagagtg tgaggcctct 700  
 aaagatcaaa acacctctgt cgtccacct cctccactc cagggagctg 750  
 tggatcatgt ggtgtgtgga acatcagcaa accgtctgtg gtcagctca 800  
 actggagagg gttttcttat ctatatgtgt cttggggtag ggattactct 850  
 ccccgagcat caaacaagag actgtattgt gtggcgccat tgaatacaga 900

tgggagactg ttggagtatt atagactgta caacacactg gatgatttgc 950  
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 ggtacagcag tttaacaaca caacatgtac gtcaacatgt acaacaccgg 1050  
 gaatatttgc agagttaaac tgaccaccaa cagattgct gtgactcaaa 1100  
 ctctccctaa tgctgcctat aataaccgct ttcatatgc taatgttgct 1150  
 tggcaagata ttgactttgc tgtggatgag aatggattgt gggttattta 1200  
 ttcaactgaa gccagcactg gtaacatggt gattagtaaa ctcaatgaca 1250  
 ccacacttca ggtgctaaac acttggtata ccaagcagta taaaccatct 1300  
 gcttctaacg ccttcatggt atgtggggtt ctgtatgcc cccgtactat 1350  
 gaacaccaga acagaagaga ttttttacta ttatgacaca aacacaggga 1400  
 aagagggcaa actagacatt gtaatgcata agatgcagga aaaagtgcag 1450  
 agcattaact ataacccttt tgaccagaaa ctttatgtct ataacgatgg 1500  
 ttacctctgc aattatgac tttctgtctt gcagaagccc cagtaagctg 1550  
 tttaggagtt agggtgaaag agaaaatggt tgttgaaaaa atagtcttct 1600  
 ccacttactt agatatctgc aggggtgtct aaaagtgtgt tcatttttga 1650  
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 cttgatttgg tgagttctct tgggaatcat ctgcctcttc aggcgcattt 1750  
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 ggaaatatg ccaatgact agtcctcacc catgtagcac cactaattct 1950  
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 attctacac tgtaaagtgc tgagttttat ggagagaggc ctttttatgc 2150  
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 agaaaatctg atggcagtga caaagtgcta gcatttattg ttatctaata 2500



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aaaa 2854

<210> 67  
<211> 510  
<212> PRT  
<213> Homo sapiens

<400> 67  
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20 25 30  
Ser Pro Gly Phe Ser Ser Phe Pro Gly Val Asp Ser Ser Ser Ser  
35 40 45  
Phe Ser Ser Ser Ser Arg Ser Gly Ser Ser Ser Arg Ser Leu  
50 55 60  
Gly Ser Gly Gly Ser Val Ser Gln Leu Phe Ser Asn Phe Thr Gly  
65 70 75  
Ser Val Asp Asp Arg Gly Thr Cys Gln Cys Ser Val Ser Leu Pro  
80 85 90  
Asp Thr Thr Phe Pro Val Asp Arg Val Glu Arg Leu Glu Phe Thr  
95 100 105  
Ala His Val Leu Ser Gln Lys Phe Glu Lys Glu Leu Ser Lys Val  
110 115 120  
Arg Glu Tyr Val Gln Leu Ile Ser Val Tyr Glu Lys Lys Leu Leu  
125 130 135  
Asn Leu Thr Val Arg Ile Asp Ile Met Glu Lys Asp Thr Ile Ser  
140 145 150  
Tyr Thr Glu Leu Asp Phe Glu Leu Ile Lys Val Glu Val Lys Glu  
155 160 165  
Met Glu Lys Leu Val Ile Gln Leu Lys Glu Ser Phe Gly Gly Ser  
170 175 180  
Ser Glu Ile Val Asp Gln Leu Glu Val Glu Ile Arg Asn Met Thr  
185 190 195  
Leu Leu Val Glu Lys Leu Glu Thr Leu Asp Lys Asn Asn Val Leu  
200 205 210

Ala	Ile	Arg	Arg	Glu	Ile	Val	Ala	Leu	Lys	Thr	Lys	Leu	Lys	Glu
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Cys	Glu	Ala	Ser	Lys	Asp	Gln	Asn	Thr	Pro	Val	Val	His	Pro	Pro
				230					235					240
Pro	Thr	Pro	Gly	Ser	Cys	Gly	His	Gly	Gly	Val	Val	Asn	Ile	Ser
				245					250					255
Lys	Pro	Ser	Val	Val	Gln	Leu	Asn	Trp	Arg	Gly	Phe	Ser	Tyr	Leu
				260					265					270
Tyr	Gly	Ala	Trp	Gly	Arg	Asp	Tyr	Ser	Pro	Gln	His	Pro	Asn	Lys
				275					280					285
Gly	Leu	Tyr	Trp	Val	Ala	Pro	Leu	Asn	Thr	Asp	Gly	Arg	Leu	Leu
				290					295					300
Glu	Tyr	Tyr	Arg	Leu	Tyr	Asn	Thr	Leu	Asp	Asp	Leu	Leu	Leu	Tyr
				305					310					315
Ile	Asn	Ala	Arg	Glu	Leu	Arg	Ile	Thr	Tyr	Gly	Gln	Gly	Ser	Gly
				320					325					330
Thr	Ala	Val	Tyr	Asn	Asn	Asn	Met	Tyr	Val	Asn	Met	Tyr	Asn	Thr
				335					340					345
Gly	Asn	Ile	Ala	Arg	Val	Asn	Leu	Thr	Thr	Asn	Thr	Ile	Ala	Val
				350					355					360
Thr	Gln	Thr	Leu	Pro	Asn	Ala	Ala	Tyr	Asn	Asn	Arg	Phe	Ser	Tyr
				365					370					375
Ala	Asn	Val	Ala	Trp	Gln	Asp	Ile	Asp	Phe	Ala	Val	Asp	Glu	Asn
				380					385					390
Gly	Leu	Trp	Val	Ile	Tyr	Ser	Thr	Glu	Ala	Ser	Thr	Gly	Asn	Met
				395					400					405
Val	Ile	Ser	Lys	Leu	Asn	Asp	Thr	Thr	Leu	Gln	Val	Leu	Asn	Thr
				410					415					420
Trp	Tyr	Thr	Lys	Gln	Tyr	Lys	Pro	Ser	Ala	Ser	Asn	Ala	Phe	Met
				425					430					435
Val	Cys	Gly	Val	Leu	Tyr	Ala	Thr	Arg	Thr	Met	Asn	Thr	Arg	Thr
				440					445					450
Glu	Glu	Ile	Phe	Tyr	Tyr	Tyr	Asp	Thr	Asn	Thr	Gly	Lys	Glu	Gly
				455					460					465
Lys	Leu	Asp	Ile	Val	Met	His	Lys	Met	Gln	Glu	Lys	Val	Gln	Ser
				470					475					480
Ile	Asn	Tyr	Asn	Pro	Phe	Asp	Gln	Lys	Leu	Tyr	Val	Tyr	Asn	Asp
				485					490					495
Gly	Tyr	Leu	Leu	Asn	Tyr	Asp	Leu	Ser	Val	Leu	Gln	Lys	Pro	Gln
				500					505					510

<210> 68  
 <211> 410  
 <212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 206, 217, 387

<223> unknown base

<400> 68

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ggtgaacatc agcaaaccgt ctgtgggtca gctcaactgg agagggtttt 150  
cttatctata tggtgcttgg ggtagggatt actctccoca gcattccaaac 200  
aaaggnatgt attggngngc gccattgaat acagatggga gactgttggg 250  
gtattataga ctgtacaacc cactggatga tttgctattg tatataaatg 300  
ctcgagagtt gcggatcacc tatggccaag gtagtggtag agcagtttac 350  
aacaacaaca tgtacgtcaa catgtacaac accgggnata ttgccagagt 400  
taacctgacc 410

<210> 69

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 69

agctgtggtc atggtggtgt ggtg 24

<210> 70

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

ctaccttggc cataggtgat ccgc 24

<210> 71

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 71

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<210> 72

<211> 3127

<212> DNA

<213> Homo sapiens

<400> 72

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tggggctgtg ctccatggcg agctggatac catgtttgtg tggaaagtcc 150  
ccgtgtttgc tatgccgatg ctgtcctagt ggaacaaact ccactgtaac 200  
tagattgac tatgcacttt tcttgcttgt tggagtatgt gtactttgtg 250  
taatgttgat accaggaatg gaagaacaac tgaataagat tcttggattt 300  
tgtgagaatg agaaagggtg tgtcccttgt aacattttgg ttggctataa 350  
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cacaatggat tttggttctt taaatttgct gcagcaattg caattattat 500  
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<210> 73  
 <211> 453  
 <212> PRT  
 <213> Homo sapiens

<400> 73

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Cys	Leu	Cys	Gly	Ser	Ala	Pro	Cys	Leu	Leu	Cys	Arg	Cys	Cys	Pro	20	25	30	30
Ser	Gly	Asn	Asn	Ser	Thr	Val	Thr	Arg	Leu	Ile	Tyr	Ala	Leu	Phe	35	40	45	45
Leu	Leu	Val	Gly	Val	Cys	Val	Ala	Cys	Val	Met	Leu	Ile	Pro	Gly	50	55	60	60
Met	Glu	Glu	Gln	Leu	Asn	Lys	Ile	Pro	Gly	Phe	Cys	Glu	Asn	Glu	65	70	75	75
Lys	Gly	Val	Val	Pro	Cys	Asn	Ile	Leu	Val	Gly	Tyr	Lys	Ala	Val	80	85	90	90
Tyr	Arg	Leu	Cys	Phe	Gly	Leu	Ala	Met	Phe	Tyr	Leu	Leu	Leu	Ser	95	100	105	105
Leu	Leu	Met	Ile	Lys	Val	Lys	Ser	Ser	Ser	Asp	Pro	Arg	Ala	Ala	110	115	120	120
Val	His	Asn	Gly	Phe	Trp	Phe	Phe	Lys	Phe	Ala	Ala	Ala	Ile	Ala	125	130	135	135
Ile	Ile	Ile	Gly	Ala	Phe	Phe	Ile	Pro	Glu	Gly	Thr	Phe	Thr	Thr	140	145	150	150
Val	Trp	Phe	Tyr	Val	Gly	Met	Ala	Gly	Ala	Phe	Cys	Phe	Ile	Leu	155	160	165	165
Ile	Gln	Leu	Val	Leu	Leu	Ile	Asp	Phe	Ala	His	Ser	Trp	Asn	Glu	170	175	180	180
Ser	Trp	Val	Glu	Lys	Met	Glu	Glu	Gly	Asn	Ser	Arg	Cys	Trp	Tyr	185	190	195	195
Ala	Ala	Leu	Leu	Ser	Ala	Thr	Ala	Leu	Asn	Tyr	Leu	Leu	Ser	Leu	200	205	210	210
Val	Ala	Ile	Val	Leu	Phe	Phe	Val	Tyr	Tyr	Thr	His	Pro	Ala	Ser	215	220	225	225
Cys	Ser	Glu	Asn	Lys	Ala	Phe	Ile	Ser	Val	Asn	Met	Leu	Leu	Cys	230	235	240	240
Val	Gly	Ala	Ser	Val	Met	Ser	Ile	Leu	Pro	Lys	Ile	Gln	Glu	Ser	245	250	255	255
Gln	Pro	Arg	Ser	Gly	Leu	Leu	Gln	Ser	Ser	Val	Ile	Thr	Val	Tyr	260	265	270	270
Thr	Met	Tyr	Leu	Thr	Trp	Ser	Ala	Met	Thr	Asn	Glu	Pro	Glu	Thr	275	280	285	285

Asn Cys Asn Pro Ser Leu Leu Ser Ile Ile Gly Tyr Asn Thr Thr  
 290 295 300  
 Ser Thr Val Pro Lys Glu Gly Gln Ser Val Gln Trp Trp His Ala  
 305 310 315  
 Gln Gly Ile Ile Gly Leu Ile Leu Phe Leu Leu Cys Val Phe Tyr  
 320 325 330  
 Ser Ser Ile Arg Thr Ser Asn Asn Ser Gln Val Asn Lys Leu Thr  
 335 340 345  
 Leu Thr Ser Asp Glu Ser Thr Leu Ile Glu Asp Gly Gly Ala Arg  
 350 355 360  
 Ser Asp Gly Ser Leu Glu Asp Gly Asp Asp Val His Arg Ala Val  
 365 370 375  
 Asp Asn Glu Arg Asp Gly Val Thr Tyr Ser Tyr Ser Phe Phe His  
 380 385 390  
 Phe Met Leu Phe Leu Ala Ser Leu Tyr Ile Met Met Thr Leu Thr  
 395 400 405  
 Asn Trp Ser Arg Tyr Glu Pro Ser Arg Glu Met Lys Ser Gln Trp  
 410 415 420  
 Thr Ala Val Trp Val Lys Ile Ser Ser Ser Trp Ile Gly Ile Val  
 425 430 435  
 Leu Tyr Val Trp Thr Leu Val Ala Pro Leu Val Leu Thr Asn Arg  
 440 445 450  
 Asp Phe Asp

<210> 74  
 <211> 480  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 48, 163  
 <223> unknown base

<400> 74  
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 ataccatgtt tgtgtggaag tgcccctgtt ttgctatgcc gatgctgtcc 150  
 tagtggaac aantccactg taactagatt gatctatgca cttttcttgc 200  
 ttgttgtagt atgtgtagct tgtgtaatgt tgataccagg aatggaagaa 250  
 caactgaata agattcctgg attttgtgag aatgagaaag gtgttgtccc 300  
 ttgtaacatt ttggttggtc ataaagctgt atatcgtttg tgctttggtt 350  
 tggctatgtt ctatcttctt ctctctttac taatgatcaa agtgaagagt 400

agcagtgatg ctagagctgc agtgcacaat ggattttggt tctttaaatt 450  
tgctgcagca attgcaatta ttattggggc 480

<210> 75  
<211> 438  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 32, 65, 92, 121, 142, 154, 170, 293, 315, 323  
<223> unknown base

<400> 75  
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tgctgtccta gtgaaacaa ntccactgta attagattga tntatgcact 150  
tttnttgctt gttggagtan gtgtagcttg tgtaatgttg ataccaggaa 200  
tggaagaaca actgaataag attcctggat tttgtgagaa tgagaaaggt 250  
gttgtccctt gtaacatttt gggtggctat aaagctgtat atngttttgtg 300  
ctttggtttg gctangttct atnttcttct ctctttacta atgatcaaaag 350  
tgaagtagtg cagtgatcct agagctgcag tgcacaatgg attttggttt 400  
tttaaatttg ctgcagcaat tgcaattatt attggggc 438

<210> 76  
<211> 473  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 48  
<223> unknown base

<400> 76  
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gtttgtgtgg aagtgccccg tgtttgctat gccgatgctg tcctagtggg 150  
aacaactcca ctgtaactag attgatctat gcacttttct tgcttgttgg 200  
agtatgtgta gcttgtgtaa tgttgatacc aggaatggaa gaacaactga 250  
ataagattoc tggattttgt gagaatgaga aaggtgttgt cccttgtaac 300  
attttggttg gctataaagc tgtatatogt ttgtgctttg gtttggtat 350  
gttctatctt ctctctctt tactaatgat caaagtgaag agtagcagtg 400  
atcctagagc tgcagtgcac aatggatttt gggtctttaa atttgctgca 450  
gcaattgcaa ttattatttg ggc 473



<210> 77  
<211> 666  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 21, 111  
<223> unknown base

<400> 77  
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caggattgga ngaacaactg aataagattc ctggattttt gtgagaatga 150  
gaaagggtgt gtccccctgt aacatttttg gttggctata aagctgtata 200  
tcgtttgtgc tttggtttgg ctatgttcta tcttcttctc tctttactaa 250  
tgatcaaagt gaagagtagc agtgatccta gagctgcagt gcacaatgga 300  
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cttcattcca gaaggaaactt ttacaactgt gtggttttat gtaggcatgg 400  
cagggtgcctt ttgtttcatc ctcatacaac tagtcttact tattgatttt 450  
gcacattcat ggaatgaatc gtgggttgaa aaaatggaag aagggaaactc 500  
gagatgttgg tatgcagcct tgttatcagc tacagctctg aattatctgc 550  
tgtctttagt tgctatcgtc ctgttctttg tctactacac tcattccagcc 600  
agttgttcag aaaacaaggc gttcatcagt gtcaacatgc tcctctgcgt 650  
tgggtcttct gtaatg 666

<210> 78  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 78  
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<210> 79  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 79  
gtcaacatgc tcctctgc 18

<210> 80  
<211> 26

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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 80
aatccattgt gcactgcagc tctagg 26

<210> 81
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 81
gagcatgccca ccactggact gac 23

<210> 82
<211> 54
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<213> Artificial Sequence

<220>
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gccgatgctg tcctagtggg aacaactcca ctgtaactag attgatctat 50
gcac 54

<210> 83
<211> 3906
<212> DNA
<213> Homo sapiens

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cgcgaggctt tcggcaaagg cagtcgagtg tttgcagacc gggcgagtc 150
ctgtgaaagc agataaaaga aaacatttat taacgtgtca ttacgagggg 200
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gacgcaactt gagactccc catcccaaaa gaagcaccag atcagcaaaa 600

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 <211> 867  
 <212> PRT  
 <213> Homo sapiens

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 Leu Lys Gly Arg Phe Gln Arg Asp Arg Arg Asn Ile Arg Pro Asn 45  
 35 40  
 Ile Ile Leu Val Leu Thr Asp Asp Gln Asp Val Glu Leu Gly Ser 60  
 50 55  
 Met Gln Val Met Asn Lys Thr Arg Arg Ile Met Glu Gln Gly Gly 75  
 65 70  
 Ala His Phe Ile Asn Ala Phe Val Thr Thr Pro Met Cys Cys Pro 90  
 80 85  
 Ser Arg Ser Ser Ile Leu Thr Gly Lys Tyr Val His Asn His Asn 105  
 95 100  
 Thr Tyr Thr Asn Asn Glu Asn Cys Ser Ser Pro Ser Trp Gln Ala 120  
 110 115  
 Gln His Glu Ser Arg Thr Phe Ala Val Tyr Leu Asn Ser Thr Gly 135  
 125 130  
 Tyr Arg Thr Ala Phe Phe Gly Lys Tyr Leu Asn Glu Tyr Asn Gly 150  
 140 145  
 Ser Tyr Val Pro Pro Gly Trp Lys Glu Trp Val Gly Leu Leu Lys 165  
 155 160  
 Asn Ser Arg Phe Tyr Asn Tyr Thr Leu Cys Arg Asn Gly Val Lys 180  
 170 175  
 Glu Lys His Gly Ser Asp Tyr Ser Lys Asp Tyr Leu Thr Asp Leu 195  
 185 190  
 Ile Thr Asn Asp Ser Val Ser Phe Phe Arg Thr Ser Lys Lys Met 210  
 200 205  
 Tyr Pro His Arg Pro Val Leu Met Val Ile Ser His Ala Ala Pro 225  
 215 220  
 His Gly Pro Glu Asp Ser Ala Pro Gln Tyr Ser Arg Leu Phe Pro 240  
 230 235  
 Asn Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn 255  
 245 250

Pro Asp Lys His	Trp	Ile Met Arg Tyr	Thr Gly Pro Met Lys	Pro
	260		265	270
Ile His Met Glu	Phe Thr Asn Met Leu	Gln Arg Lys Arg Leu	Gln	
	275		280	285
Thr Leu Met Ser	Val Asp Asp Ser Met	Glu Thr Ile Tyr Asn	Met	
	290		295	300
Leu Val Glu Thr	Gly Glu Leu Asp Asn	Thr Tyr Ile Val Tyr	Thr	
	305		310	315
Ala Asp His Gly	Tyr His Ile Gly Gln	Phe Gly Leu Val Lys	Gly	
	320		325	330
Lys Ser Met Pro	Tyr Glu Phe Asp Ile	Arg Val Pro Phe Tyr	Val	
	335		340	345
Arg Gly Pro Asn	Val Glu Ala Gly Cys	Leu Asn Pro His Ile	Val	
	350		355	360
Leu Asn Ile Asp	Leu Ala Pro Thr Ile	Leu Asp Ile Ala Gly	Leu	
	365		370	375
Asp Ile Pro Ala	Asp Met Asp Gly Lys	Ser Ile Leu Lys Leu	Leu	
	380		385	390
Asp Thr Glu Arg	Pro Val Asn Arg Phe	His Leu Lys Lys Lys	Met	
	395		400	405
Arg Val Trp Arg	Asp Ser Phe Leu Val	Glu Arg Gly Lys Leu	Leu	
	410		415	420
His Lys Arg Asp	Asn Asp Lys Val Asp	Ala Gln Glu Glu Asn	Phe	
	425		430	435
Leu Pro Lys Tyr	Gln Arg Val Lys Asp	Leu Cys Gln Arg Ala	Glu	
	440		445	450
Tyr Gln Thr Ala	Cys Glu Gln Leu Gly	Gln Lys Trp Gln Cys	Val	
	455		460	465
Glu Asp Ala Thr	Gly Lys Leu Lys Leu	His Lys Cys Lys Gly	Pro	
	470		475	480
Met Arg Leu Gly	Gly Ser Arg Ala Leu	Ser Asn Leu Val Pro	Lys	
	485		490	495
Tyr Tyr Gly Gln	Gly Ser Glu Ala Cys	Thr Cys Asp Ser Gly	Asp	
	500		505	510
Tyr Lys Leu Ser	Leu Ala Gly Arg Arg	Lys Lys Leu Phe Lys	Lys	
	515		520	525
Lys Tyr Lys Ala	Ser Tyr Val Arg Ser	Arg Ser Ile Arg Ser	Val	
	530		535	540
Ala Ile Glu Val	Asp Gly Arg Val Tyr	His Val Gly Leu Gly	Asp	
	545		550	555
Ala Ala Gln Pro	Arg Asn Leu Thr Lys	Arg His Trp Pro Gly	Ala	
	560		565	570

Pro Glu Asp Gln Asp Asp Lys Asp Gly Gly Asp Phe Ser Gly Thr  
 575 580 585  
 Gly Gly Leu Pro Asp Tyr Ser Ala Ala Asn Pro Ile Lys Val Thr  
 590 595 600  
 His Arg Cys Tyr Ile Leu Glu Asn Asp Thr Val Gln Cys Asp Leu  
 605 610 615  
 Asp Leu Tyr Lys Ser Leu Gln Ala Trp Lys Asp His Lys Leu His  
 620 625 630  
 Ile Asp His Glu Ile Glu Thr Leu Gln Asn Lys Ile Lys Asn Leu  
 635 640 645  
 Arg Glu Val Arg Gly His Leu Lys Lys Lys Arg Pro Glu Glu Cys  
 650 655 660  
 Asp Cys His Lys Ile Ser Tyr His Thr Gln His Lys Gly Arg Leu  
 665 670 675  
 Lys His Arg Gly Ser Ser Leu His Pro Phe Arg Lys Gly Leu Gln  
 680 685 690  
 Glu Lys Asp Lys Val Trp Leu Leu Arg Glu Gln Lys Arg Lys Lys  
 695 700 705  
 Lys Leu Arg Lys Leu Leu Lys Arg Leu Gln Asn Asn Asp Thr Cys  
 710 715 720  
 Ser Met Pro Gly Leu Thr Cys Phe Thr His Asp Asn Gln His Trp  
 725 730 735  
 Gln Thr Ala Pro Phe Trp Thr Leu Gly Pro Phe Cys Ala Cys Thr  
 740 745 750  
 Ser Ala Asn Asn Asn Thr Tyr Trp Cys Met Arg Thr Ile Asn Glu  
 755 760 765  
 Thr His Asn Phe Leu Phe Cys Glu Phe Ala Thr Gly Phe Leu Glu  
 770 775 780  
 Tyr Phe Asp Leu Asn Thr Asp Pro Tyr Gln Leu Met Asn Ala Val  
 785 790 795  
 Asn Thr Leu Asp Arg Asp Val Leu Asn Gln Leu His Val Gln Leu  
 800 805 810  
 Met Glu Leu Arg Ser Cys Lys Gly Tyr Lys Gln Cys Asn Pro Arg  
 815 820 825  
 Thr Arg Asn Met Asp Leu Asp Gly Gly Ser Tyr Glu Gln Tyr Arg  
 830 835 840  
 Gln Phe Gln Arg Arg Lys Trp Pro Glu Met Lys Arg Pro Ser Ser  
 845 850 855  
 Lys Ser Leu Gly Gln Leu Trp Glu Gly Trp Glu Gly  
 860 865

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 <210> 86  
 <211> 18  
 <212> DNA  
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 <223> Synthetic oligonucleotide probe  
 <400> 86  
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 <223> Synthetic oligonucleotide probe  
 <400> 87  
 aagggcctgc aagagaag 18  
 <210> 88  
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 <400> 88  
 cactgggaca actgtggg 18  
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 <400> 89  
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 <211> 21  
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 <220>  
 <223> Synthetic oligonucleotide probe  
 <400> 90  
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<210> 91  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 91  
tagtacttgg gcacgaggtt ggag 24

<210> 92  
<211> 24  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 92  
tcataccaac tgctggtcat tggc 24

<210> 93  
<211> 45  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 93  
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<210> 94  
<211> 971  
<212> DNA  
<213> Homo sapiens

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tgggcctcct ggggagcaca gccctcgtgg gatggatcac aggtgctgct 150  
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acggcaggac tgtgacgtgg agaggaaccg tacagctgca gggggaaacc 250  
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tgtcgccggt gcctgtggac agcagctgcc cctgccctcc catctgttcc 500  
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gaacgagggg aacaatagac tggggccttg tccagctgca tttgcatggc 600

atgccccagt gtactatggc agcagagaat ggaggaacac tgggtctgca 650  
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 ccctgagaat gtccttttgg ttgggagaag gcagtgtgag gctgcacagt 900  
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 aaaaaaaaaa aaaaaaaaaa a 971

<210> 95  
 <211> 115  
 <212> PRT  
 <213> Homo sapiens

<400> 95  
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 Cys Leu Phe His Gly Arg Gln Asp Cys Asp Val Glu Arg Asn Arg  
 35 40 45  
 Thr Ala Ala Gly Gly Asn Arg Val Arg Arg Ala Gln Pro Trp Pro  
 50 55 60  
 Phe Arg Arg Arg Gly His Leu Gly Ile Phe His His His Arg His  
 65 70 75  
 Pro Gly His Val Ser His Val Pro Asn Val Gly Leu His His His  
 80 85 90  
 His His Pro Arg His Thr Pro His His Leu His His His His His  
 95 100 105  
 Pro His Arg His His Pro Arg His Ala Arg  
 110 115

<210> 96  
 <211> 1312  
 <212> DNA  
 <213> Homo sapiens

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 gctgacgctg ctggcctttg ccgggtactc agggctactg gctggggctg 150  
 aagtgagtgc tgggtcacc cccatccgca acgtcactgt ggctacaag 200  
 ttccacatgg ggctctatgg tgagactggg cggtctttca ctgagagctg 250  
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acatggtgcc ccctgataag tgccgatgtg ccgtgggcag catcctgagt 350  
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<210> 97  
 <211> 313  
 <212> FRT  
 <213> Homo sapiens

<400> 97  
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 Leu Ala Gly Val Glu Val Ser Ala Gly Ser Pro Ile Arg Asn  
 35 40 45  
 Val Thr Val Ala Tyr Lys Phe His Met Gly Leu Tyr Gly Glu Thr  
 50 55 60  
 Gly Arg Leu Phe Thr Glu Ser Cys Ser Ile Ser Pro Lys Leu Arg  
 65 70 75

Ser Ile Ala Val Tyr Tyr Asp Asn Pro His Met Val Pro Pro Asp  
 80 85 90  
 Lys Cys Arg Cys Ala Val Gly Ser Ile Leu Ser Glu Gly Glu Glu  
 95 100 105  
 Ser Pro Ser Pro Glu Leu Ile Asp Leu Tyr Gln Lys Phe Gly Phe  
 110 115 120  
 Lys Val Phe Ser Phe Pro Ala Pro Ser His Val Val Thr Ala Thr  
 125 130 135  
 Phe Pro Tyr Thr Thr Ile Leu Ser Ile Trp Leu Ala Thr Arg Arg  
 140 145 150  
 Val His Pro Ala Leu Asp Thr Tyr Ile Lys Glu Arg Lys Leu Cys  
 155 160 165  
 Ala Tyr Pro Arg Leu Glu Ile Tyr Gln Glu Asp Gln Ile His Phe  
 170 175 180  
 Met Cys Pro Leu Ala Arg Gln Gly Asp Phe Tyr Val Pro Glu Met  
 185 190 195  
 Lys Glu Thr Glu Trp Lys Trp Arg Gly Leu Val Glu Ala Ile Asp  
 200 205 210  
 Thr Gln Val Asp Gly Thr Gly Ala Asp Thr Met Ser Asp Thr Ser  
 215 220 225  
 Ser Val Ser Leu Glu Val Ser Pro Gly Ser Arg Glu Thr Ser Ala  
 230 235 240  
 Ala Thr Leu Ser Pro Gly Ala Ser Ser Arg Gly Trp Asp Asp Gly  
 245 250 255  
 Asp Thr Arg Ser Glu His Ser Tyr Ser Glu Ser Gly Ala Ser Gly  
 260 265 270  
 Ser Ser Phe Glu Glu Leu Asp Leu Glu Gly Glu Gly Pro Leu Gly  
 275 280 285  
 Glu Ser Arg Leu Asp Pro Gly Thr Glu Pro Leu Gly Thr Thr Lys  
 290 295 300  
 Trp Leu Trp Glu Pro Thr Ala Pro Glu Lys Gly Lys Glu  
 305 310

<210> 98

<211> 725

<212> DNA

<213> Homo sapiens

<400> 98

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 cccgctccat ctgctgctgc tgctgctgct cagtgcggcg gtgtgccggg 150  
 ctgaggctgg gctcgaaacc gaaagtcccg tccggaccct ccaagtggag 200  
 accctggtgg agccccaga accatgtgcc gagcccgctg cttttggaga 250

cacgcttcac atacactaca cggaagcctt ggtagatgga cgtattattg 300  
 acacctccct gaccagagac cctctggtta tagaacttgg ccaaaagcag 350  
 gtgattccag gtctggagca gagtcttctc gacatgtgtg tggagagaaa 400  
 gcgaaggcca atcattcctt ctcaacttggc ctatggaaaa cggggatttc 450  
 caccatctgt cccagcggat gcagtgtgtc agtatgacgt ggagctgatt 500  
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 tctgttaggg atggccatgg tgccagccct cctgggcctc attgggtatc 600  
 acctatacag aaaggccaat agaccctaaag tctccaaaaa gaagctcaag 650  
 gaagagaaa gaaacaagag caaaaagaaa taataataa taaattttaa 700  
 aaaacttaaa aaaaaaaaa aaaaa 725

<210> 99  
 <211> 201  
 <212> PRT  
 <213> Homo sapiens

<400> 99  
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 Thr Glu Ser Pro Val Arg Thr Leu Gln Val Glu Thr Leu Val Glu  
 35 40 45  
 Pro Pro Glu Pro Cys Ala Glu Pro Ala Ala Phe Gly Asp Thr Leu  
 50 55 60  
 His Ile His Tyr Thr Gly Ser Leu Val Asp Gly Arg Ile Ile Asp  
 65 70 75  
 Thr Ser Leu Thr Arg Asp Pro Leu Val Ile Glu Leu Gly Gln Lys  
 80 85 90  
 Gln Val Ile Pro Gly Leu Glu Gln Ser Leu Asp Met Cys Val  
 95 100 105  
 Gly Glu Lys Arg Arg Ala Ile Ile Pro Ser His Leu Ala Tyr Gly  
 110 115 120  
 Lys Arg Gly Phe Pro Pro Ser Val Pro Ala Asp Ala Val Val Gln  
 125 130 135  
 Tyr Asp Val Glu Leu Ile Ala Leu Ile Arg Ala Asn Tyr Trp Leu  
 140 145 150  
 Lys Leu Val Lys Gly Ile Leu Pro Leu Val Gly Met Ala Met Val  
 155 160 165  
 Pro Ala Leu Leu Gly Leu Ile Gly Tyr His Leu Tyr Arg Lys Ala  
 170 175 180  
 Asn Arg Pro Lys Val Ser Lys Lys Lys Leu Lys Glu Glu Lys Arg

Asn Lys Ser Lys Lys Lys  
200

<210> 100  
<211> 705  
<212> DNA  
<213> Homo sapiens

<400> 100  
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cgctccatct gctgctgctg ctgctgctca gtgcggcggt gtgccgggct 150  
gaggctgggc tcgaaaccga aagtcccgtc cggaccctcc aagtggagac 200  
cctgggtggag cccccagaac catgtgccga gcccgctgct tttggagaca 250  
cgcttcacat acactacacg ggaagccttg tagatggacg tattattgac 300  
acctccctga ccagagaccc tcgggttata gaacttgccc aaaagcaggt 350  
gattccaggt ctggagcaga gtcttctcga catgtgtgtg ggagagaagc 400  
gaagggaact cattccttct cacttgccct atggaaaacg gggatttcca 450  
ccatctgtcc cagcggatgc agtgggtgcag tatgacgtgg agctgattgc 500  
actaatccga gccaaactact ggctaaagct ggtgaagggc attttgcttc 550  
tggtagggat ggccatgggt ccaccctcct gggcctcatt gggtatcacc 600  
tatacagaaa ggccaataga cccaaagtct ccaaaaagaa gctcaaggaa 650  
gagaaacgaa acaagagcaa aaagaaataa taaataataa attttaaaaa 700  
actta 705

<210> 101  
<211> 543  
<212> DNA  
<213> Homo sapiens

<400> 101  
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cacgggaagc ttggtagatg gacgtattat tgacacctcc ctgaccagag 150  
acctctctgt tatagaactt ggccaaaagc aggtgattcc aggtctggag 200  
cagagtcttc tcgacatgtg tgtgggagag aagcgaaggc caatcattcc 250  
ttctcacttg gcctatggaa aacggggatt tccaccatct gtcccagcgg 300  
atgcagtgtg gcagtatgac gtggagctga ttgcactaat ccgagccaac 350  
tactggctaa agctgggtgaa gggcattttg cctctggtag ggtggccat 400

gggtccagcc ctctctggcc tcattgggta tcacctatac agaaaggcca 450  
 atagacccaa agtctccaaa aagaagctca aggaagagaa acgaacaacg 500  
 agcaaaaaga aataataaat aataaat tttt aaaaaactta aaa 543

<210> 102  
 <211> 1316  
 <212> DNA  
 <213> Homo sapiens

<400> 102  
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 ccactgcacg acggggcttg actgacctga aaaaaatgtc tggatttcta 150  
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<211> 157

<212> PRT

<213> Homo sapiens

<400> 103

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			20						25					30
Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Ile	Ile	Asp	Ala	Ala	Val	Ile
			35						40					45
Tyr	Pro	Thr	Met	Lys	Asp	Phe	Asn	His	Ser	Tyr	His	Ala	Cys	Gly
			50						55					60
Val	Ile	Ala	Thr	Ile	Ala	Phe	Leu	Met	Ile	Asn	Ala	Val	Ser	Asn
			65						70					75
Gly	Gln	Val	Arg	Gly	Asp	Ser	Tyr	Ser	Glu	Gly	Cys	Leu	Gly	Gln
			80						85					90
Thr	Gly	Ala	Arg	Ile	Trp	Leu	Phe	Val	Gly	Phe	Met	Leu	Ala	Phe
			95						100					105
Gly	Ser	Leu	Ile	Ala	Ser	Met	Trp	Ile	Leu	Phe	Gly	Gly	Tyr	Val
			110						115					120
Ala	Lys	Glu	Lys	Asp	Ile	Val	Tyr	Pro	Gly	Ile	Ala	Val	Phe	Phe
			125						130					135
Gln	Asn	Ala	Phe	Ile	Phe	Phe	Gly	Gly	Leu	Val	Phe	Lys	Phe	Gly
			140						145					150
Arg	Thr	Glu	Asp	Leu	Trp	Gln								
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<210> 104

<211> 545

<212> DNA

<213> Homo sapiens

<400> 104

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agcgcaatac tattgcttcc attgctgctg gtgtactatt ttttacaggc 200  
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ggttgtctgg gtcaaacagg tgctgcatt tggcttttcg ttggtttcat 400



gttggccttt ggatctctga ttgcatctat gtggattcct tttggagggt 450  
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 cagaatgcct tcactctttt tggagggtcg gtttttaagt ttggc 545

<210> 105  
 <211> 490  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 31, 39, 108, 145, 179, 219, 412, 479  
 <223> unknown base

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 tgggtgtaata ttttttacag gctggtggat tatcatagat gcagntgtta 150  
 tttatccac catgaaagat ttcaaccant cataccatgc ctgtggtgtt 200  
 atagcaacca tagccttont aatgattaat gcagtatcga atggacaagt 250  
 ccgaggtgat agttacagtg aaggttgttt ggtgcaaaca ggtgctcgca 300  
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 atgtggattc tttttggagg ttatgttgc aaagaaaaa acatagtata 400  
 ccctggaatt gntgtatttt tccagaatgc cttcatcttt tttggagggc 450  
 tggtttttaa gtttggccgc actgaagant tatggcagtg 490

<210> 106  
 <211> 466  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 26, 38, 81, 115, 207, 329, 380, 446, 449  
 <223> unknown base

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 acagggtggt ggattatcat agatgcagct gttatttacc ccaccatgaa 200  
 agattttnaac cactcattacc atgcctgttg tgttatagca accatagcct 250  
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 agtgaagggt gtttgggtca aacaggtgnt cgcatttggc ttttcgttg 350  
 tttcatgttg gcttttgat ttctgattgn attctatgcg gattcttctt 400

ggaggttatg ttgctaaaga aaaagacata gtataccctg gaattntcnt 450

atttttccag aatgcc 466

<210> 107

<211> 377

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 52, 67, 70, 78, 105, 144, 150, 209, 266, 268, 282, 310, 331, 356

<223> unknown base

<400> 107

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ttatnataga tgcagctgtt atttatccca ccatgaaaga ttnaaccan 150

tcataccatg cctgtggtgt tatagcaacc atagccttcc taatgattaa 200

tgcagtatng aatggacaag tccgaggtga tagttacagt gaaggtgtgt 250

tgggtcaaac aggtgntngc atttggttt tngttggttt catgttgcc 300

tttgatctn tgattgcatt tatgtggatt ntttttgag gttatgtgtc 350

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<210> 108

<211> 552

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 12, 25, 65, 130, 437, 537

<223> unknown base

<400> 108

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ggactgcacct gaaaaaaatg tttggatttn tagagggtctt gagatgctca 150

gaatgcattg actgggggga aaagcgcaat actattgctt ccattgtctgc 200

tgggtgacta ttttttacag gctggtggat taccatagat gcagctgtta 250

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ccgaggtgat agttacagt aaggttgtct gggtaaca ggtgtcgcga 400

tttggtcttt cgttggtttc atgttggtct ttggatntct gattgcattc 450

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<210> 110  
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<223> Synthetic oligonucleotide probe

<400> 110  
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<210> 111  
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<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

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<212> DNA  
<213> Homo sapiens

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ccgaatcctt tctccgaaga tgtcaaacgg cccccagcgc ccctggtaac 150  
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<210> 113  
 <211> 610  
 <212> PRT  
 <213> Homo sapiens

<400> 113  
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 Asn Pro Phe Ser Glu Asp Val Lys Arg Pro Pro Ala Pro Leu Val  
 35 40 45  
 Thr Asp Lys Glu Ala Arg Lys Lys Val Leu Lys Gln Ala Phe Ser  
 50 55 60  
 Ala Asn Gln Val Pro Glu Lys Leu Asp Val Val Val Ile Gly Ser  
 65 70 75  
 Gly Phe Gly Gly Leu Ala Ala Ala Ala Ile Leu Ala Lys Ala Gly  
 80 85 90  
 Lys Arg Val Leu Val Leu Glu Gln His Thr Lys Ala Gly Gly Cys  
 95 100 105

Cys	His	Thr	Phe	Gly	Lys	Asn	Gly	Leu	Glu	Phe	Asp	Thr	Gly	Ile
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His	Tyr	Ile	Gly	Arg	Met	Glu	Glu	Gly	Ser	Ile	Gly	Arg	Phe	Ile
				125					130					135
Leu	Asp	Gln	Ile	Thr	Glu	Gly	Gln	Leu	Asp	Trp	Ala	Pro	Leu	Ser
				140					145					150
Ser	Pro	Phe	Asp	Ile	Met	Val	Leu	Glu	Gly	Pro	Asn	Gly	Arg	Lys
				155					160					165
Glu	Tyr	Pro	Met	Tyr	Ser	Gly	Glu	Lys	Ala	Tyr	Ile	Gln	Gly	Leu
				170					175					180
Lys	Glu	Lys	Phe	Pro	Gln	Glu	Glu	Ala	Ile	Ile	Asp	Lys	Tyr	Ile
				185					190					195
Lys	Leu	Val	Lys	Val	Val	Ser	Ser	Gly	Ala	Pro	His	Ala	Ile	Leu
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Leu	Lys	Phe	Leu	Pro	Leu	Pro	Val	Val	Gln	Leu	Leu	Asp	Arg	Cys
				215					220					225
Gly	Leu	Leu	Thr	Arg	Phe	Ser	Pro	Phe	Leu	Gln	Ala	Ser	Thr	Gln
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Ser	Leu	Ala	Glu	Val	Leu	Gln	Gln	Leu	Gly	Ala	Ser	Ser	Glu	Leu
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Gln	Ala	Val	Leu	Ser	Tyr	Ile	Phe	Pro	Thr	Tyr	Gly	Val	Thr	Pro
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Asn	His	Ser	Ala	Phe	Ser	Met	His	Ala	Leu	Leu	Val	Asn	His	Tyr
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Met	Lys	Gly	Gly	Phe	Tyr	Pro	Arg	Gly	Gly	Ser	Ser	Glu	Ile	Ala
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Phe	His	Thr	Ile	Pro	Val	Ile	Gln	Arg	Ala	Gly	Gly	Ala	Val	Leu
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Thr	Lys	Ala	Thr	Val	Gln	Ser	Val	Leu	Leu	Asp	Ser	Ala	Gly	Lys
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Ala	Cys	Gly	Val	Ser	Val	Lys	Lys	Gly	His	Glu	Leu	Val	Asn	Ile
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Tyr	Cys	Pro	Ile	Val	Val	Ser	Asn	Ala	Gly	Leu	Phe	Asn	Thr	Tyr
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Glu	His	Leu	Leu	Pro	Gly	Asn	Ala	Arg	Cys	Leu	Pro	Gly	Val	Lys
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Gln	Gln	Leu	Gly	Thr	Val	Arg	Pro	Gly	Leu	Gly	Met	Thr	Ser	Val
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Phe	Ile	Cys	Leu	Arg	Gly	Thr	Lys	Glu	Asp	Leu	His	Leu	Pro	Ser
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Thr	Asn	Tyr	Tyr	Val	Tyr	Tyr	Asp	Thr	Asp	Met	Asp	Gln	Ala	Met
				410					415					420

Glu Arg Tyr Val Ser Met Pro Arg Glu Glu Ala Ala Glu His Ile  
 425 430  
 Pro Leu Leu Phe Phe Ala Phe Pro Ser Ala Lys Asp Pro Thr Trp  
 440 445 450  
 Glu Asp Arg Phe Pro Gly Arg Ser Thr Met Ile Met Leu Ile Pro  
 455 460 465  
 Thr Ala Tyr Glu Trp Phe Glu Glu Trp Gln Ala Glu Leu Lys Gly  
 470 475 480  
 Lys Arg Gly Ser Asp Tyr Glu Thr Phe Lys Asn Ser Phe Val Glu  
 485 490 495  
 Ala Ser Met Ser Val Val Leu Lys Leu Phe Pro Gln Leu Glu Gly  
 500 505 510  
 Lys Val Glu Ser Val Thr Ala Gly Ser Pro Leu Thr Asn Gln Phe  
 515 520 525  
 Tyr Leu Ala Ala Pro Arg Gly Ala Cys Tyr Gly Ala Asp His Asp  
 530 535 540  
 Leu Gly Arg Leu His Pro Cys Val Met Ala Ser Leu Arg Ala Gln  
 545 550 555  
 Ser Pro Ile Pro Asn Leu Tyr Leu Thr Gly Gln Asp Ile Phe Thr  
 560 565 570  
 Cys Gly Leu Val Gly Ala Leu Gln Gly Ala Leu Leu Cys Ser Ser  
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 Ala Ile Leu Lys Arg Asn Leu Tyr Ser Asp Leu Lys Asn Leu Asp  
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 Ser Arg Ile Arg Ala Gln Lys Lys Lys Asn  
 605 610

<210> 114  
 <211> 1701  
 <212> DNA  
 <213> Homo sapiens

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<210> 115

<211> 301

<212> PRT

<213> Homo sapiens

<400> 115

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Lys Asp His Thr	Thr Ala Gly Arg Val	Val Ala Gly Gln Ile Phe
50	55	60
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Glu Asp Ser Leu	Lys Ser Gln Glu Gly Glu	Ser Val Thr Glu Asp
80	85	90
Ile Ser Phe Leu	Glu Ser Pro Asn Pro Glu	Asn Lys Asp Tyr Glu
95	100	105
Glu Pro Lys Lys	Val Arg Lys Pro Ala Leu	Thr Ala Ile Glu Gly
110	115	120
Thr Ala His Gly	Glu Pro Cys His Phe Pro	Phe Leu Phe Leu Asp
125	130	135
Lys Glu Tyr Asp	Glu Cys Thr Ser Asp Gly	Arg Glu Asp Gly Arg
140	145	150
Leu Trp Cys Ala	Thr Thr Tyr Asp Tyr Lys	Ala Asp Glu Lys Trp
155	160	165
Gly Phe Cys Glu	Thr Glu Glu Glu Ala Ala	Lys Arg Arg Gln Met
170	175	180
Gln Glu Ala Glu	Met Met Tyr Gln Thr Gly	Met Lys Ile Leu Asn
185	190	195
Gly Ser Asn Lys	Lys Ser Gln Lys Arg Glu	Ala Tyr Arg Tyr Leu
200	205	210
Gln Lys Ala Ala	Ser Met Asn His Thr Lys	Ala Leu Glu Arg Val
215	220	225
Ser Tyr Ala Leu	Leu Phe Gly Asp Tyr Leu	Pro Gln Asn Ile Gln
230	235	240
Ala Ala Arg Glu	Met Phe Glu Lys Leu Thr	Glu Glu Gly Ser Pro
245	250	255
Lys Gly Gln Thr	Ala Leu Gly Phe Leu Tyr	Ala Ser Gly Leu Gly
260	265	270
Val Asn Ser Ser	Gln Ala Lys Ala Leu Val	Tyr Tyr Thr Phe Gly
275	280	285
Ala Leu Gly Gly	Asn Leu Ile Ala His Met	Val Leu Val Ser Arg
290	295	300

Leu

<210> 116  
 <211> 584  
 <212> DNA  
 <213> Homo sapiens  
 <400> 116

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 agctggatgc actgctgggc tccccaggcc aagtggctca actctctgc 200  
 acgtcacgcc cccagcacgt caccatcagg gactacggtg tgtctggta 250  
 ccagcagcgg gcaggcagtg cccctcgata tctctctac taccgctcgg 300  
 agggaggatca ccacggcct gctgacatcc ccgatcgatt ctggcgagcc 350  
 aaggatgagg cccacaatgc ctgtgtcttc accattatgc ccgtgcagcc 400  
 tgaagacgac gcggattact actgctctgt tggctacggc tttagtccct 450  
 aggggtgggg tgtgagatgg gtgcctcccc tctgctcccc atttctgccc 500  
 ctgaccttgg gtccctttta aactttctct gagccttgct tcccctctgt 550  
 aaaatggggtt aataatattc aacatgtcaa caac 584

<210> 117  
 <211> 123  
 <212> PRT  
 <213> Homo sapiens

<400> 117  
 Met Ala Cys Arg Cys Leu Ser Phe Leu Leu Met Gly Thr Phe Leu  
 1 5 10 15  
 Ser Val Ser Gln Thr Val Leu Ala Gln Leu Asp Ala Leu Leu Val  
 20 25 30  
 Phe Pro Gly Gln Val Ala Gln Leu Ser Cys Thr Leu Ser Pro Gln  
 35 40 45  
 His Val Thr Ile Arg Asp Tyr Gly Val Ser Trp Tyr Gln Gln Arg  
 50 55 60  
 Ala Gly Ser Ala Pro Arg Tyr Leu Leu Tyr Tyr Arg Ser Glu Glu  
 65 70 75  
 Asp His His Arg Pro Ala Asp Ile Pro Asp Arg Phe Ser Ala Ala  
 80 85 90  
 Lys Asp Glu Ala His Asn Ala Cys Val Leu Thr Ile Ser Pro Val  
 95 100 105  
 Gln Pro Glu Asp Asp Ala Asp Tyr Tyr Cys Ser Val Gly Tyr Gly  
 110 115 120  
 Phe Ser Pro

<210> 118  
 <211> 3402  
 <212> DNA  
 <213> Homo sapiens

<400> 118

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 cgccccgggg ggcatgacc gcggagcgca cgccgcgggc cggccctga 100  
 cccccgcgcc cggccgtga ccccccgcc gaggtccgga caggccgaga 150  
 tgacgcgcgag cccctgttg ctgctctgc tgcgcgcgt getgtgggg 200  
 gccttccac cggccgcgc cgcccgaggc ccccaaaaga tggcggacaa 250  
 ggtggtccca cggcaggtg ccgggctggg ccgactgtg cggctgcagt 300  
 gcccagtga gggggaccgc ccgccgtga ccatgtggac caaggatggc 350  
 cgcaccatcc acagcggtg gagccgttc cgcgtgtgc cgcaggggct 400  
 gaagtggaag caggtggagc gggaggatg cgcgtgtac gtgtcaag 450  
 ccaccaacgc cttcggcgc ctgagcgtca actacacct cgtcgtgtg 500  
 gatgacatta gccagggaa ggagagcctg gggccgcaca gctcctctg 550  
 ggtcaagag gaccccgcca gccagcagt ggacgcagc cgcttcacac 600  
 agccctcaa gatgagcgc cgggtgatg caccgcccgt gggtagctcc 650  
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 caaggtgat gtgatccgc ggaccggtc caagccgtg ctcacaggca 900  
 cgcacccgt gaacacgag gtggacttc gggggaccac gtccttcag 950  
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 ggtctccgc agccccccag cacttactg gcccaggccc agttgtggc 1550  
 cctaagttg accccaaact ctacacagac atccacacac acacacacac 1600



gaaggaagac tgggttcag ggactgtggt ctctctggg gcccgggacc 3250  
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 ccacccccca cccactgtc gtgtggccc cagatctctg taattttatg 3350  
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 aa 3402

<210> 119  
 <211> 504  
 <212> PRT  
 <213> Homo sapiens

<400> 119  
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu  
 1 5 10 15  
 Leu Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys  
 20 25 30  
 Met Ala Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg  
 35 40 45  
 Thr Val Arg Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu  
 50 55 60  
 Thr Met Trp Thr Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser  
 65 70 75  
 Arg Phe Arg Val Leu Pro Gln Gly Leu Lys Val Lys Gln Val Glu  
 80 85 90  
 Arg Glu Asp Ala Gly Val Tyr Val Cys Lys Ala Thr Asn Gly Phe  
 95 100 105  
 Gly Ser Leu Ser Val Asn Tyr Thr Leu Val Val Leu Asp Asp Ile  
 110 115 120  
 Ser Pro Gly Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly  
 125 130 135  
 Gln Glu Asp Pro Ala Ser Gln Gln Trp Ala Arg Pro Arg Phe Thr  
 140 145 150  
 Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly  
 155 160 165  
 Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro  
 170 175 180  
 Asp Ile Thr Trp Met Lys Asp Asp Gln Ala Leu Thr Arg Pro Glu  
 185 190 195  
 Ala Ala Glu Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn  
 200 205 210  
 Leu Arg Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn  
 215 220 225  
 Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile Gln  
 230 235 240

Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	
				245					250					255	
Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	
				260					265					270	
Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	
				275					280					285	
Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	
				290					295					300	
Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	
				305					310					315	
Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	
				320					325					330	
Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	
				335					340					345	
Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	
				350					355					360	
Pro	Pro	Gly	Pro	Pro	Val	Ala	Ser	Ser	Ser	Ser	Ala	Thr	Ser	Leu	
				365					370					375	
Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	
				380					385					390	
Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro	
				395					400					405	
Cys	Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro	Gly	His	Arg	Pro	Pro	
				410					415					420	
Gly	Thr	Ala	Arg	Asp	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	
				425					430					435	
Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys	Glu	Glu	His	
				440					445					450	
Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly	Pro	Val	
				455					460					465	
Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His	Thr	
				470					475					480	
His	Thr	His	Thr	His	Ser	His	Thr	His	Ser	His	Val	Glu	Gly	Lys	
				485					490					495	
Val	His	Gln	His	Ile	His	Tyr	Gln	Cys							
				500											

<210> 120

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

cgagatgacg ccgagccccc 20

<210> 121

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

cggttcgaca cgcggcaggt g 21

<210> 122

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 122

tgtctgctct gctgccgcg ctgctgctgg gggccttccc gcccg 45

<210> 123

<211> 4420

<212> DNA

<213> Homo sapiens

<400> 123

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cccaggggac cgcattccag agtcagtgc tctgtgaagc acccacatct 100  
acctcttgcc acgttccac gggcttgggg gaaagatggt ggggaccaag 150  
gcttgggtgt tctccttct ggtcctggaa gtcacatctg tgttggggag 200  
acagacgatg ctcaccagc cagtaagaag agtccagcct ggggaagaaga 250  
acccagcat ctttgccaag cctgccgaca ccctggagag ccctggtgag 300  
tggaacaacat ggttcaacat cgactaccca ggccgggaagg gcgactatga 350  
gcggctggac gccattcgct tctactatgg ggaccgtgta tgtgccgtc 400  
ccctgcggct agaggctcgg accactgact ggacacctgc gggcagcaact 450  
ggccaggtgg tccatggtag tcccgtgag ggtttctggt gcctcaacag 500  
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tctccctgga gcaagtgtc agctgctgt ggtcagactg gggtcagac 650  
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gcgaagaggg tcagcactgc atgggccagg actgtacagc ctgtgacctg 750  
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 tactctgtat ttcgaaaaaa 4420

<210> 124  
 <211> 1184  
 <212> PRT  
 <213> Homo sapiens

<400> 124  
 Met Val Gly Thr Lys Ala Trp Val Phe Ser Phe Leu Val Leu Glu  
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 Val Thr Ser Val Leu Gly Arg Gln Thr Met Leu Thr Gln Ser Val  
 20 25 30  
 Arg Arg Val Gln Pro Gly Lys Lys Asn Pro Ser Ile Phe Ala Lys  
 35 40 45  
 Pro Ala Asp Thr Leu Glu Ser Pro Gly Glu Trp Thr Thr Trp Phe  
 50 55 60  
 Asn Ile Asp Tyr Pro Gly Gly Lys Gly Asp Tyr Glu Arg Leu Asp  
 65 70 75  
 Ala Ile Arg Phe Tyr Tyr Gly Asp Arg Val Cys Ala Arg Pro Leu  
 80 85 90  
 Arg Leu Glu Ala Arg Thr Thr Asp Trp Thr Pro Ala Gly Ser Thr  
 95 100 105  
 Gly Gln Val Val His Gly Ser Pro Arg Glu Gly Phe Trp Cys Leu  
 110 115 120  
 Asn Arg Glu Gln Arg Pro Gly Gln Asn Cys Ser Asn Tyr Thr Val  
 125 130 135  
 Arg Phe Leu Cys Pro Pro Gly Ser Leu Arg Arg Asp Thr Glu Arg  
 140 145 150  
 Ile Trp Ser Pro Trp Ser Pro Trp Ser Lys Cys Ser Ala Ala Cys  
 155 160 165  
 Gly Gln Thr Gly Val Gln Thr Arg Thr Arg Ile Cys Leu Ala Glu  
 170 175 180  
 Met Val Ser Leu Cys Ser Glu Ala Ser Glu Glu Gly Gln His Cys  
 185 190 195  
 Met Gly Gln Asp Cys Thr Ala Cys Asp Leu Thr Cys Pro Met Gly  
 200 205 210

Gln Val Asn Ala	Asp Cys Asp Ala Cys	Met Cys Gln Asp Phe	Met
	215	220	225
Leu His Gly Ala	Val Ser Leu Pro Gly	Gly Ala Pro Ala Ser	Gly
	230	235	240
Ala Ala Ile Tyr	Leu Leu Thr Lys Thr	Pro Lys Leu Leu Thr	Gln
	245	250	255
Thr Asp Ser Asp	Gly Arg Phe Arg Ile	Pro Gly Leu Cys Pro	Asp
	260	265	270
Gly Lys Ser Ile	Leu Lys Ile Thr Lys	Val Lys Phe Ala Pro	Ile
	275	280	285
Val Leu Thr Met	Pro Lys Thr Ser Leu	Lys Ala Ala Thr Ile	Lys
	290	295	300
Ala Glu Phe Val	Arg Ala Glu Thr Pro	Tyr Met Val Met Asn	Pro
	305	310	315
Glu Thr Lys Ala	Arg Arg Ala Gly Gln	Ser Val Ser Leu Cys	Cys
	320	325	330
Lys Ala Thr Gly	Lys Pro Arg Pro Asp	Lys Tyr Phe Trp Tyr	His
	335	340	345
Asn Asp Thr Leu	Leu Asp Pro Ser Leu	Tyr Lys His Glu Ser	Lys
	350	355	360
Leu Val Leu Arg	Lys Leu Gln Gln His	Gln Ala Gly Glu Tyr	Phe
	365	370	375
Cys Lys Ala Gln	Ser Asp Ala Gly Ala	Val Lys Ser Lys Val	Ala
	380	385	390
Gln Leu Ile Val	Thr Ala Ser Asp Glu	Thr Pro Cys Asn Pro	Val
	395	400	405
Pro Glu Ser Tyr	Leu Ile Arg Leu Pro	His Asp Cys Phe Gln	Asn
	410	415	420
Ala Thr Asn Ser	Phe Tyr Tyr Asp Val	Gly Arg Cys Pro Val	Lys
	425	430	435
Thr Cys Ala Gly	Gln Gln Asp Asn Gly	Ile Arg Cys Arg Asp	Ala
	440	445	450
Val Gln Asn Cys	Cys Gly Ile Ser Lys	Thr Glu Glu Arg Glu	Ile
	455	460	465
Gln Cys Ser Gly	Tyr Thr Leu Pro Thr	Lys Val Ala Lys Glu	Cys
	470	475	480
Ser Cys Gln Arg	Cys Thr Glu Thr Arg	Ser Ile Val Arg Gly	Arg
	485	490	495
Val Ser Ala Ala	Asp Asn Gly Glu Pro	Met Arg Phe Gly His	Val
	500	505	510
Tyr Met Gly Asn	Ser Arg Val Ser Met	Thr Gly Tyr Lys Gly	Thr
	515	520	525

Phe Thr Leu His Val Pro Gln Asp Thr Glu Arg Leu Val Leu Thr	530	535	540
Phe Val Asp Arg Leu Gln Lys Phe Val Asn Thr Thr Lys Val Leu	545	550	555
Pro Phe Asn Lys Lys Gly Ser Ala Val Phe His Glu Ile Lys Met	560	565	570
Leu Arg Arg Lys Glu Pro Ile Thr Leu Glu Ala Met Glu Thr Asn	575	580	585
Ile Ile Pro Leu Gly Glu Val Val Gly Glu Asp Pro Met Ala Glu	590	595	600
Leu Glu Ile Pro Ser Arg Ser Phe Tyr Arg Gln Asn Gly Glu Pro	605	610	615
Tyr Ile Gly Lys Val Lys Ala Ser Val Thr Phe Leu Asp Pro Arg	620	625	630
Asn Ile Ser Thr Ala Thr Ala Ala Gln Thr Asp Leu Asn Phe Ile	635	640	645
Asn Asp Glu Gly Asp Thr Phe Pro Leu Arg Thr Tyr Gly Met Phe	650	655	660
Ser Val Asp Phe Arg Asp Glu Val Thr Ser Glu Pro Leu Asn Ala	665	670	675
Gly Lys Val Lys Val His Leu Asp Ser Thr Gln Val Lys Met Pro	680	685	690
Glu His Ile Ser Thr Val Lys Leu Trp Ser Leu Asn Pro Asp Thr	695	700	705
Gly Leu Trp Glu Glu Glu Gly Asp Phe Lys Phe Glu Asn Gln Arg	710	715	720
Arg Asn Lys Arg Glu Asp Arg Thr Phe Leu Val Gly Asn Leu Glu	725	730	735
Ile Arg Glu Arg Arg Leu Phe Asn Leu Asp Val Pro Glu Ser Arg	740	745	750
Arg Cys Phe Val Lys Val Arg Ala Tyr Arg Ser Glu Arg Phe Leu	755	760	765
Pro Ser Glu Gln Ile Gln Gly Val Val Ile Ser Val Ile Asn Leu	770	775	780
Glu Pro Arg Thr Gly Phe Leu Ser Asn Pro Arg Ala Trp Gly Arg	785	790	795
Phe Asp Ser Val Ile Thr Gly Pro Asn Gly Ala Cys Val Pro Ala	800	805	810
Phe Cys Asp Asp Gln Ser Pro Asp Ala Tyr Ser Ala Tyr Val Leu	815	820	825
Ala Ser Leu Ala Gly Glu Glu Leu Gln Ala Val Glu Ser Ser Pro	830	835	840

Lys	Phe	Asn	Pro	Asn	Ala	Ile	Gly	Val	Pro	Gln	Pro	Tyr	Leu	Asn	
				845					850					855	
Lys	Leu	Asn	Tyr	Arg	Arg	Thr	Asp	His	Glu	Asp	Pro	Arg	Val	Lys	
				860					865					870	
Lys	Thr	Ala	Phe	Gln	Ile	Ser	Met	Ala	Lys	Pro	Arg	Pro	Asn	Ser	
				875					880					885	
Ala	Glu	Glu	Ser	Asn	Gly	Pro	Ile	Tyr	Ala	Phe	Glu	Asn	Leu	Arg	
				890					895					900	
Ala	Cys	Glu	Glu	Ala	Pro	Pro	Ser	Ala	Ala	His	Phe	Arg	Phe	Tyr	
				905					910					915	
Gln	Ile	Glu	Gly	Asp	Arg	Tyr	Asp	Tyr	Asn	Thr	Val	Pro	Phe	Asn	
				920					925					930	
Glu	Asp	Asp	Pro	Met	Ser	Trp	Thr	Glu	Asp	Tyr	Leu	Ala	Trp	Trp	
				935					940					945	
Pro	Lys	Pro	Met	Glu	Phe	Arg	Ala	Cys	Tyr	Ile	Lys	Val	Lys	Ile	
				950					955					960	
Val	Gly	Pro	Leu	Glu	Val	Asn	Val	Arg	Ser	Arg	Asn	Met	Gly	Gly	
				965					970					975	
Thr	His	Arg	Arg	Thr	Val	Gly	Lys	Leu	Tyr	Gly	Ile	Arg	Asp	Val	
				980					985					990	
Arg	Ser	Thr	Arg	Asp	Arg	Asp	Gln	Pro	Asn	Val	Ser	Ala	Ala	Cys	
				995					1000					1005	
Leu	Glu	Phe	Lys	Cys	Ser	Gly	Met	Leu	Tyr	Asp	Gln	Asp	Arg	Val	
				1010					1015					1020	
Asp	Arg	Thr	Leu	Val	Lys	Val	Ile	Pro	Gln	Gly	Ser	Cys	Arg	Arg	
				1025					1030					1035	
Ala	Ser	Val	Asn	Pro	Met	Leu	His	Glu	Tyr	Leu	Val	Asn	His	Leu	
				1040					1045					1050	
Pro	Leu	Ala	Val	Asn	Asn	Asp	Thr	Ser	Glu	Tyr	Thr	Met	Leu	Ala	
				1055					1060					1065	
Pro	Leu	Asp	Pro	Leu	Gly	His	Asn	Tyr	Gly	Ile	Tyr	Thr	Val	Thr	
				1070					1075					1080	
Asp	Gln	Asp	Pro	Arg	Thr	Ala	Lys	Glu	Ile	Ala	Leu	Gly	Arg	Cys	
				1085					1090					1095	
Phe	Asp	Gly	Thr	Ser	Asp	Gly	Ser	Ser	Arg	Ile	Met	Lys	Ser	Asn	
				1100					1105					1110	
Val	Gly	Val	Ala	Leu	Thr	Phe	Asn	Cys	Val	Glu	Arg	Gln	Val	Gly	
				1115					1120					1125	
Arg	Gln	Ser	Ala	Phe	Gln	Tyr	Leu	Gln	Ser	Thr	Pro	Ala	Gln	Ser	
				1130					1135					1140	
Pro	Ala	Ala	Gly	Thr	Val	Gln	Gly	Arg	Val	Pro	Ser	Arg	Arg	Gln	
				1145					1150					1155	

Gln Arg Ala Ser Arg Gly Gly Gln Arg Gln Gly Gly Val Val Ala  
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Ser Leu Arg Phe Pro Arg Val Ala Gln Gln Pro Leu Ile Asn  
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<210> 126  
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<220>  
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 <212> DNA  
 <213> Homo sapiens

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 ttgggatctg ctttgaggtc ccattctcat ttaaaaaaaa atacagagac 150  
 ctacctaccg gtacgcatac atacatatgt gtatatatat gtaaactaga 200  
 caaagatcgc agatcataaa gcaagctctg ctttagtttc caagaagatt 250  
 acaagaatt tagagatgta ttgtcaaga tccctgtcga ttcattgcct 300  
 ttgggttacg gtgtcctcag tgatgcagcc ctaccctttg gtttggggac 350  
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<210> 129

<211> 438

<212> PRT

<213> Homo sapiens

<400> 129

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Val	Ser	Ser	Val	Met	Gln	Pro	Tyr	Pro	Leu	Val	Trp	Gly	His	Tyr	20	25	30	
Asp	Leu	Cys	Lys	Thr	Gln	Ile	Tyr	Thr	Glu	Gly	Lys	Val	Trp		35	40	45	
Asp	Tyr	Met	Ala	Cys	Gln	Pro	Glu	Ser	Thr	Asp	Met	Thr	Lys	Tyr	50	55	60	
Leu	Lys	Val	Lys	Leu	Asp	Pro	Pro	Asp	Ile	Thr	Cys	Gly	Asp	Pro	65	70	75	
Pro	Glu	Thr	Phe	Cys	Ala	Met	Gly	Asn	Pro	Tyr	Met	Cys	Asn	Asn	80	85	90	
Glu	Cys	Asp	Ala	Ser	Thr	Pro	Glu	Leu	Ala	His	Pro	Pro	Glu	Leu	95	100	105	
Met	Phe	Asp	Phe	Glu	Gly	Arg	His	Pro	Ser	Thr	Phe	Trp	Gln	Ser	110	115	120	
Ala	Thr	Trp	Lys	Glu	Tyr	Pro	Lys	Pro	Leu	Gln	Val	Asn	Ile	Thr				



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Leu Ser Trp Ser	Lys Thr Ile Glu Leu	Thr Asp Asn Ile Val	Ile		
	140		145		150
Thr Phe Glu Ser	Gly Arg Pro Asp Gln	Met Ile Leu Glu Lys	Ser		
	155		160		165
Leu Asp Tyr Gly	Arg Thr Trp Gln Pro	Tyr Gln Tyr Tyr Ala	Thr		
	170		175		180
Asp Cys Leu Asp	Ala Phe His Met Asp	Pro Lys Ser Val Lys	Asp		
	185		190		195
Leu Ser Gln His	Thr Val Leu Glu Ile	Ile Cys Thr Glu Glu	Tyr		
	200		205		210
Ser Thr Gly Tyr	Thr Thr Asn Ser Lys	Ile Ile His Phe Glu	Ile		
	215		220		225
Lys Asp Arg Phe	Ala Leu Phe Ala Gly	Pro Arg Leu Arg Asn	Met		
	230		235		240
Ala Ser Leu Tyr	Gly Gln Leu Asp Thr	Thr Lys Lys Leu Arg	Asp		
	245		250		255
Phe Phe Thr Val	Thr Asp Leu Arg Ile	Arg Leu Leu Arg Pro	Ala		
	260		265		270
Val Gly Glu Ile	Phe Val Asp Glu Leu	His Leu Ala Arg Tyr	Phe		
	275		280		285
Tyr Ala Ile Ser	Asp Ile Lys Val Arg	Gly Arg Cys Lys Cys	Asn		
	290		295		300
Leu His Ala Thr	Val Cys Val Tyr Asp	Asn Ser Lys Leu Thr	Cys		
	305		310		315
Glu Cys Glu His	Asn Thr Thr Gly Pro	Asp Cys Gly Lys Cys	Lys		
	320		325		330
Lys Asn Tyr Gln	Gly Arg Pro Trp Ser	Pro Gly Ser Tyr Leu	Pro		
	335		340		345
Ile Pro Lys Gly	Thr Ala Asn Thr Cys	Ile Pro Ser Ile Ser	Ser		
	350		355		360
Ile Gly Thr Asn	Val Cys Asp Asn Glu	Leu Leu His Cys Gln	Asn		
	365		370		375
Gly Gly Thr Cys	His Asn Asn Val Arg	Cys Leu Cys Pro Ala	Ala		
	380		385		390
Tyr Thr Gly Ile	Leu Cys Glu Lys Leu	Arg Cys Glu Glu Ala	Gly		
	395		400		405
Ser Cys Gly Ser	Asp Ser Gly Gln Gly	Ala Pro Pro His Gly	Thr		
	410		415		420
Pro Ala Leu Leu	Leu Leu Thr Thr Leu	Leu Gly Thr Ala Ser	Pro		
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Leu Val Phe					

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 <213> Homo sapiens  
  
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 ccgggcgagg tgtcctcatg acttctcttg tggaccatgt ccgtgatctt 150  
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<210> 135

<211> 228

<212> PRT

<213> Homo sapiens

<400> 135

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				20					25					30

Leu	Glu	Trp	Arg	Arg	Arg	Leu	Lys	Ser	Leu	Ala	Leu	Arg	Leu	Ala
				35					40					45

Gln	Tyr	Pro	Gly	Arg	Gly	Ser	Ala	Glu	Gly	Cys	Asp	Phe	Ser	Ile	
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His	Phe	Ser	Ser	Phe	Gly	Asp	Val	Ala	Cys	Met	Ala	Ile	Cys	Ser	
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Cys	Gln	Cys	Pro	Ala	Ala	Met	Ala	Phe	Cys	Phe	Leu	Glu	Thr	Leu	
				80					85					90	
Trp	Trp	Glu	Phe	Thr	Ala	Ser	Tyr	Asp	Thr	Thr	Cys	Ile	Gly	Leu	
				95					100					105	
Ala	Ser	Arg	Pro	Tyr	Ala	Phe	Leu	Glu	Phe	Asp	Ser	Ile	Ile	Gln	
				110					115					120	
Lys	Val	Lys	Trp	His	Phe	Asn	Tyr	Val	Ser	Ser	Ser	Gln	Met	Glu	
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Cys	Ser	Leu	Glu	Lys	Ile	Gln	Glu	Glu	Leu	Lys	Leu	Gln	Pro	Pro	
				140					145					150	
Ala	Val	Leu	Thr	Leu	Glu	Asp	Thr	Asp	Val	Ala	Asn	Gly	Val	Met	
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Asn	Gly	His	Thr	Pro	Met	His	Leu	Glu	Pro	Ala	Pro	Asn	Phe	Arg	
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Met	Glu	Pro	Val	Thr	Ala	Leu	Gly	Ile	Leu	Ser	Leu	Ile	Leu	Asn	
				185					190					195	
Ile	Met	Cys	Ala	Ala	Leu	Asn	Leu	Ile	Arg	Gly	Val	His	Leu	Ala	
				200					205					210	
Glu	His	Ser	Leu	Gln	Asp	Pro	Arg	Ser	Trp	Phe	Cys	Trp	Leu	Asp	
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Gln	Thr	Ser													

<210> 136  
 <211> 239  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 39, 61, 143, 209  
 <223> unknown base

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<213> Homo sapiens

<400> 137

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gcctcactgc tgttctgggc catccccata gccatgttta catgatttga 2100  
tgtgcaatag ggtggggtag gggcagggaagg actgtggc cagggcaggc 2150  
tcgggagata gattgtctcc cttgcctctg gccagcaga gcctaagcac 2200  
tgtgtctatc tggaggggct ttggaccacc tgaagacca aggggatagg 2250  
gaggaggagg cttcagccat cagcaataaa gttgatccca gggaaaaaaa 2300

<210> 138

<211> 489

<212> PRT

<213> Homo sapiens

<400> 138

Met Glu Ala Pro Asp Tyr Glu Val Leu Ser Val Arg Glu Gln Leu  
1 5 10 15

Phe His Glu Arg Ile Arg Glu Cys Ile Ile Ser Thr Leu Leu Phe  
20 25 30

Ala Thr Leu Tyr Ile Leu Cys His Ile Phe Leu Thr Arg Phe Lys  
35 40 45

Lys Pro Ala Glu Phe Thr Thr Val Asp Asp Glu Asp Ala Thr Val  
50 55 60

Asn Lys Ile Ala Leu Glu Leu Cys Thr Phe Thr Leu Ala Ile Ala  
65 70 75

Leu Gly Ala Val Leu Leu Leu Pro Phe Ser Ile Ile Ser Asn Glu  
80 85 90

Val Leu Leu Ser Leu Pro Arg Asn Tyr Tyr Ile Gln Trp Leu Asn  
95 100 105

Gly Ser Leu Ile His Gly Leu Trp Asn Leu Val Phe Leu Phe Pro  
110 115 120

Asn Leu Ser Leu Ile Phe Leu Met Pro Phe Ala Tyr Phe Phe Thr

	125		130		135
Glu Ser Glu Gly Phe Ala Gly Ser Arg Lys Gly Val Leu Gly Arg	140		145		150
Val Tyr Glu Thr Val Val Met Leu Met Leu Leu Thr Leu Leu Val	155		160		165
Leu Gly Met Val Trp Val Ala Ser Ala Ile Val Asp Lys Asn Lys	170		175		180
Ala Asn Arg Glu Ser Leu Tyr Asp Phe Trp Glu Tyr Tyr Leu Pro	185		190		195
Tyr Leu Tyr Ser Cys Ile Ser Phe Leu Gly Val Leu Leu Leu Leu	200		205		210
Val Cys Thr Pro Leu Gly Leu Ala Arg Met Phe Ser Val Thr Gly	215		220		225
Lys Leu Leu Val Lys Pro Arg Leu Leu Glu Asp Leu Glu Glu Gln	230		235		240
Leu Tyr Cys Ser Ala Phe Glu Glu Ala Ala Leu Thr Arg Arg Ile	245		250		255
Cys Asn Pro Thr Ser Cys Trp Leu Pro Leu Asp Met Glu Leu Leu	260		265		270
His Arg Gln Val Leu Ala Leu Gln Thr Gln Arg Val Leu Leu Glu	275		280		285
Lys Arg Arg Lys Ala Ser Ala Trp Gln Arg Asn Leu Gly Tyr Pro	290		295		300
Leu Ala Met Leu Cys Leu Leu Val Leu Thr Gly Leu Ser Val Leu	305		310		315
Ile Val Ala Ile His Ile Leu Glu Leu Leu Ile Asp Glu Ala Ala	320		325		330
Met Pro Arg Gly Met Gln Gly Thr Ser Leu Gly Gln Val Ser Phe	335		340		345
Ser Lys Leu Gly Ser Phe Gly Ala Val Ile Gln Val Val Leu Ile	350		355		360
Phe Tyr Leu Met Val Ser Ser Val Val Gly Phe Tyr Ser Ser Pro	365		370		375
Leu Phe Arg Ser Leu Arg Pro Arg Trp His Asp Thr Ala Met Thr	380		385		390
Gln Ile Ile Gly Asn Cys Val Cys Leu Leu Val Leu Ser Ser Ala	395		400		405
Leu Pro Val Phe Ser Arg Thr Leu Gly Leu Thr Arg Phe Asp Leu	410		415		420
Leu Gly Asp Phe Gly Arg Phe Asn Trp Leu Gly Asn Phe Tyr Ile	425		430		435
Val Phe Leu Tyr Asn Ala Ala Phe Ala Gly Leu Thr Thr Leu Cys					

440	445	450
Leu Val Lys Thr Phe Thr Ala Ala Val Arg Ala Glu Leu Ile Arg		
455	460	465
Ala Phe Gly Leu Asp Arg Leu Pro Leu Pro Val Ser Gly Phe Pro		
470	475	480
Gln Ala Ser Arg Lys Thr Gln His Gln		
485		

<210> 139  
 <211> 294  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 53, 57  
 <223> unknown base

<400> 139  
 ggctgccgag ggaaggcccc ttgggttggt cttggttgct tggcgggcgc 50  
 ggntttontcc cgcctcgtcc tccccggggc cagaggcacc tcggttcag 100  
 tcatgctgag cagagtatgg aagcacctga ctacgaagtg ctatcogtgc 150  
 gagaacacgt attccacgag aggatccgcg agtgattat atcaaacatt 200  
 ctgtttgcaa cactgtacat cctctgccac atcttcctga cccgcttcaa 250  
 gaagcctgct gagttcacca cagtggatga tgaagatgcc accg 294

<210> 140  
 <211> 526  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 197, 349  
 <223> unknown base

<400> 140  
 gaccgacctt aaagagtggg agcaaaggga ggacagagcc ttttaaacg 50  
 aggcggttggt gcttgcctt taaggcgggg gcgtccggac gactgtatct 100  
 gagccccaga ctgccccgag tttctgtcgc aggctgcgag gaaagggccc 150  
 taggctgggt ctggtgcttg gcggcggcgg ctctctcccc gttgtontcc 200  
 ccgggcccag aggcacctcg gcttcagtca tgctgagcag agtatggaag 250  
 cacctgacta cgaagtgtca tccgtgcgag aacagctatt ccacgagagg 300  
 atccgcgagt gtattatata aacacttctg tttgcaacac tgtacatcnt 350  
 ctgccacatc ttcctgacct gcttcaagaa gcctgctgag ttcaccacag 400  
 tggatgatga agatgccacc gtcaacaaga ttgcgctcga gctgtgcacc 450



tttacccctgg caattgccct ggggtgctgtc ctgctccctgc ccttctccat 500  
catcagcaat gaggtgctgc actccc 526

<210> 141  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 141  
gactgtatct gagccccaga ctgc 24

<210> 142  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 142  
tcagcaatga ggtgctgtc 20

<210> 143  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 143  
tgaggaagat gagggacagg ttgg 24

<210> 144  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 144  
tatggaagca cctgactacg aagtgtatc cgtgcgagaa cagctattcc 50

<210> 145  
<211> 685  
<212> DNA  
<213> Homo sapiens

<400> 145  
gatgtgctcc ttggagctgg tgtgcagtgt cctgactgta agatcaagtc 50  
caaacctgtt ttggaattga ggaacttct cttttgatct cagcccttgg 100  
tgggtccagg cttcatgctg ctgtgggtga tattactggt cctggctcct 150  
gtcagtgagc agtttgcaag gacaccagg ccattattt tctccagcc 200  
tccatggacc acagtcttcc aaggagagag agtgaccctc acttgcaagg 250

gatttcgctt ctactcacca cagaaaaaaa aatggtacca tcggtacctt 300  
 gggaagaaaa tactaagaga aaccccagac aatatccttg aggttcagga 350  
 atctggagag tacagatgcc aggccaggg ctccctctc agtagccctg 400  
 tgcacttga tttttcttca gagatgggat ttctctatgc tgcccaggct 450  
 aatgttgaac tctgggctc aagtgatctg ctacacatgg cctctcaaag 500  
 cgctgggatt acagcttcgc tgatcctgca agctccactt tctgtgttg 550  
 aaggagactc tgtggttctg aggtgccggg caaaggcgga agtaacactg 600  
 aataatacta tttaacaagaa tgataatgct ctggcattcc ttaataaaaag 650  
 aactgacttc caaaaaaaaa aaaaaaaaaa aaaaa 685

<210> 146  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<400> 146  
 Met Leu Leu Trp Val Ile Leu Leu Val Leu Ala Pro Val Ser Gly  
 1 5 10 15  
 Gln Phe Ala Arg Thr Pro Arg Pro Ile Ile Phe Leu Gln Pro Pro  
 20 25 30  
 Trp Thr Thr Val Phe Gln Gly Glu Arg Val Thr Leu Thr Cys Lys  
 35 40 45  
 Gly Phe Arg Phe Tyr Ser Pro Gln Lys Thr Lys Trp Tyr His Arg  
 50 55 60  
 Tyr Leu Gly Lys Glu Ile Leu Arg Glu Thr Pro Asp Asn Ile Leu  
 65 70 75  
 Glu Val Gln Glu Ser Gly Glu Tyr Arg Cys Gln Ala Gln Gly Ser  
 80 85 90  
 Pro Leu Ser Ser Pro Val His Leu Asp Phe Ser Ser Glu Met Gly  
 95 100 105  
 Phe Pro His Ala Ala Gln Ala Asn Val Glu Leu Leu Gly Ser Ser  
 110 115 120  
 Asp Leu Leu Thr

<210> 147  
 <211> 1621  
 <212> DNA  
 <213> Homo sapiens

<400> 147  
 cagaagagg ggctagctag ctgtctctgc ggaccaggga gacccccgcg 50  
 cccccccgt gtgaggcggc ctacacagggc cggtgggct gccgagccga 100  
 cgcgggcgcg gaggaggctg tgaggagtgt gtggaacagg acccgggaca 150

gaggaaccat ggctccgcag aacctgagca ccttttgctt gttgctgcta 200  
 tacctcatcg gggcggtgat tgcgggacga gatttctata agatcttggg 250  
 ggtgcctcga agtgccctcta taaaggatat taaaaggcc tataggaaac 300  
 tagccctcga gcttcatccc gaccggaacc ctgatgatcc acaagcccag 350  
 gagaattcc aggatctggg tgctgcttat gaggttctgt cagatagtga 400  
 gaaacggaaa cagtacgata cttatggtga agaaggatta aaagatggtc 450  
 atcagagctc ccatggagac attttttcac acttctttgg ggattttggt 500  
 ttcatgtttg gaggaacccc tegtacgcaa gacagaaata ttccaaggag 550  
 aagtgtatatt attgtagatc tagaagtac tttggaagaa gtatatgcag 600  
 gaaattttgt ggaagtagtt agaaacaaac ctgtggcaag gcaggtcctc 650  
 ggcaaacgga agtgcaattg tcggcaagag atgcggacca ccagctggg 700  
 ccctggggcg ttccaaatga ccaggagggt ggtctgcgac gaatgcccta 750  
 atgtcaaaact agtgaatgaa gaacgaacgc tggaagtaga aatagagcct 800  
 ggggtgagag acggcatgga gtaccccttt attggaagag gtgagcctca 850  
 cgtggatggg gagcctggag atttacgggt ccgaatcaaa gttgtcaagc 900  
 acccaatatt tgaaggagga ggagatgatt tgtacacaaa tgtgacaatc 950  
 tcattagtgt agtcactggt tggctttgag atggatatta ctcaactgga 1000  
 tggtcacaag gtacatatatt ccggggataa gatcaccagg ccaggagoga 1050  
 agctatggaa gaaaggggaa gggctcccca actttgacaa caacaatata 1100  
 aagggtctct tgataatcac ttttgatgtg gattttccaa aagaacagtt 1150  
 aacagaggaa gcgagagaag gtatcaaaca gctactgaaa caagggtcag 1200  
 tgcagaaggt atacaatgga ctgcaaggat attgagagtg aataaaattg 1250  
 gactttgttt aaaataagtg aataagcgat atttattatc tgcaagggtt 1300  
 ttttgtgtgt gttttgttt ttattttcaa tatgcaagtt aggccttaatt 1350  
 tttttatcta atgatcatca tgaatgaat aagagggctt aagaatttgt 1400  
 ccatttgcat tcggaaaaga atgaccagca aaaggtttac taatacctct 1450  
 ccctttgggg atttaatgtc tgggtgctgcc gcctgagttt caagaattaa 1500  
 agctgcaaga ggactccagg agcaaaagaa acacaatata gagggttgga 1550  
 gttgttagca atttcattca aaatgccaac tggagaagtc tgtttttaaa 1600  
 tacattttgt tgttattttt a 1621

<210> 148  
 <211> 358  
 <212> PRT

<213> Homo sapiens

<400> 148

Met	Ala	Pro	Gln	Asn	Leu	Ser	Thr	Phe	Cys	Leu	Leu	Leu	Tyr	
1				5					10				15	
Leu	Ile	Gly	Ala	Val	Ile	Ala	Gly	Arg	Asp	Phe	Tyr	Lys	Ile	Leu
				20					25				30	
Gly	Val	Pro	Arg	Ser	Ala	Ser	Ile	Lys	Asp	Ile	Lys	Lys	Ala	Tyr
				35					40				45	
Arg	Lys	Leu	Ala	Leu	Gln	Leu	His	Pro	Asp	Arg	Asn	Pro	Asp	Asp
				50					55				60	
Pro	Gln	Ala	Gln	Glu	Lys	Phe	Gln	Asp	Leu	Gly	Ala	Ala	Tyr	Glu
				65					70				75	
Val	Leu	Ser	Asp	Ser	Glu	Lys	Arg	Lys	Gln	Tyr	Asp	Thr	Tyr	Gly
				80					85				90	
Glu	Glu	Gly	Leu	Lys	Asp	Gly	His	Gln	Ser	Ser	His	Gly	Asp	Ile
				95					100				105	
Phe	Ser	His	Phe	Phe	Gly	Asp	Phe	Gly	Phe	Met	Phe	Gly	Gly	Thr
				110					115				120	
Pro	Arg	Gln	Gln	Asp	Arg	Asn	Ile	Pro	Arg	Gly	Ser	Asp	Ile	Ile
				125					130				135	
Val	Asp	Leu	Glu	Val	Thr	Leu	Glu	Glu	Val	Tyr	Ala	Gly	Asn	Phe
				140					145				150	
Val	Glu	Val	Val	Arg	Asn	Lys	Pro	Val	Ala	Arg	Gln	Ala	Pro	Gly
				155					160				165	
Lys	Arg	Lys	Cys	Asn	Cys	Arg	Gln	Glu	Met	Arg	Thr	Thr	Gln	Leu
				170					175				180	
Gly	Pro	Gly	Arg	Phe	Gln	Met	Thr	Gln	Glu	Val	Val	Cys	Asp	Glu
				185					190				195	
Cys	Pro	Asn	Val	Lys	Leu	Val	Asn	Glu	Glu	Arg	Thr	Leu	Glu	Val
				200					205				210	
Glu	Ile	Glu	Pro	Gly	Val	Arg	Asp	Gly	Met	Glu	Tyr	Pro	Phe	Ile
				215					220				225	
Gly	Glu	Gly	Glu	Pro	His	Val	Asp	Gly	Glu	Pro	Gly	Asp	Leu	Arg
				230					235				240	
Phe	Arg	Ile	Lys	Val	Val	Lys	His	Pro	Ile	Phe	Glu	Arg	Arg	Gly
				245					250				255	
Asp	Asp	Leu	Tyr	Thr	Asn	Val	Thr	Ile	Ser	Leu	Val	Glu	Ser	Leu
				260					265				270	
Val	Gly	Phe	Glu	Met	Asp	Ile	Thr	His	Leu	Asp	Gly	His	Lys	Val
				275					280				285	
His	Ile	Ser	Arg	Asp	Lys	Ile	Thr	Arg	Pro	Gly	Ala	Lys	Leu	Trp
				290					295				300	

Lys Lys Gly Glu Gly Leu Pro Asn Phe Asp Asn Asn Asn Ile Lys  
 305 310  
 Gly Ser Leu Ile Ile Thr Phe Asp Val Asp Phe Pro Lys Glu Gln  
 320 325  
 Leu Thr Glu Glu Ala Arg Glu Gly Ile Lys Gln Leu Leu Lys Gln  
 335 340 345  
 Gly Ser Val Gln Lys Val Tyr Asn Gly Leu Gln Gly Tyr  
 350 355

<210> 149  
 <211> 509  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> unsure  
 <222> 34, 52, 134, 142, 155, 158, 196, 217, 228, 272, 347, 410, 445,  
 482  
 <223> unknown base

<400> 149  
 tgggaccagg gaaccccggtg ccccccggtg gagngcctaa caggccggtg 50  
 gntgcgaccg aagcgcggtg cggaggaggt tttgaggatt ttggaacag 100  
 gaccgggaca gaggaaccat ggttccgcag aacntgagca cnttttgctt 150  
 gttgntgnta tacttcatcg gggcggtgat tgcggagca gatttntata 200  
 agatttttgg gtgcctngaa gtgccttnta taaaggatat taaaaaggcc 250  
 tataggaaac tagccctgca gntttatccc gaccggaacc ctgatgatcc 300  
 acaagcccag gagaaattcc aggatttggg tgctgcttat gaggttntgt 350  
 cagatagtga gaaacggaaa cagtacgata attatggtga agaaggatta 400  
 aaagatggtg atcagagctc ccatggagac attttttcac acttntttgg 450  
 ggatttttgt ttcattgttg gaggaacccc tngtcagcaa gacagaaaaa 500  
 ttccaagag 509

<210> 150  
 <211> 1532  
 <212> DNA  
 <213> Homo sapiens

<400> 150  
 ggcacgagc ggcggggcag tcgcgggatg cgcccgaggag ccacagcctg 50  
 aggccttcag gtctctgcag gtgtcgtgga ggaacctagc acctgccatc 100  
 ctcttcccca atttgccact tccagcagct ttagcccatg aggaggatgt 150  
 gaccgggact gagtcaggag ccctctgga gcatggagac tgtggtgatt 200  
 gttgccatag gtgtgtctgc caccatcttt ctggtctcgt ttgcagcctt 250  
 ggtgctggtt tgcaggcagc gctactgccg gccgcgagac ctgctgcagc 300

gctatgattc taagccatt gtggacctca ttggtgcat ggagaccag 350  
 tctgagccct ctgagttaga actggacgat gtcgttatca ccaaccccca 400  
 cattgagggc attctggaga atgaagactg gatcgaagat gcctcggtgc 450  
 tcatgtccca ctgcattgcc atcttgaaga tttgtcacac tctgacagag 500  
 aagctgtgtg ccatgacaat gggctctggg gccaaagatga agacttcagc 550  
 cagtgtcagc gacatcattg tgggtggcaa gcggatcagc ccaggggtg 600  
 atgatgttgt gaagtcgatg taccctcctg tggaccccaa actcctggac 650  
 gcacggacga ctgccctgct cctgtctgtc agtcacctgg tgcgtgtgac 700  
 aaggaatgcc tgccatctga cgggaggcct ggactggatt gaccagtctc 750  
 tgtcggtgtc tgaggagcat ttggaagtcc ttcgagaagc agccctagct 800  
 tctgagccag ataaaggcct ccagggcct gaaggcttcc tgcaggagca 850  
 gtctgcaatt tagtgcctac aggcacagcag ctagccatga aggccctgc 900  
 cgccatccct gcatggetca gcttagcctt ctacttttct ctatagagtt 950  
 agttgtttct caccgctgga gagttagct gtgtgtgat agtaaagcag 1000  
 gagatccccc tcagtttatg cctcttttgc agttgcaaac tgtggctggt 1050  
 gagtggcagt ctaatactac agttagggga gatgccatc actctctgca 1100  
 agaggagtat tgaaaactgg tggactgtca gctttattta gctcacctag 1150  
 tgttttcaag aaaattgagc caccgtctaa gaaatcaaga ggtttcacat 1200  
 taaaattaga atttctggcc tctctcgatc ggtcagaatg tgtggcaatt 1250  
 ctgatctgca ttttcagaag aggacaatca attgaaacta agtaggggtt 1300  
 tcttcttttg gcaagacttg tactctctca cctggcctgt ttcatttatt 1350  
 tgtattattc gcttggctcc tgaggcgtct gggctctccc tctcccttgc 1400  
 aggtttgggt ttgaagctga ggaactacaa agttgatgat ttctttttta 1450  
 tctttatgcc tgcaatttta cctagctacc actaggtgga tagtaatttt 1500  
 atacttatgt ttccctcaaa aaaaaaaaaa aa 1532

<210> 151  
 <211> 226  
 <212> PRT  
 <213> Homo sapiens

<400> 151  
 Met Glu Thr Val Val Ile Val Ala Ile Gly Val Leu Ala Thr Ile  
 1 5 10 15  
 Phe Leu Ala Ser Phe Ala Ala Leu Val Leu Val Cys Arg Gln Arg  
 20 25 30  
 Tyr Cys Arg Pro Arg Asp Leu Leu Gln Arg Tyr Asp Ser Lys Pro

	35	40	45
Ile Val Asp Leu Ile Gly Ala Met Glu Thr Gln Ser Glu Pro Ser	50	55	60
Glu Leu Glu Leu Asp Asp Val Val Ile Thr Asn Pro His Ile Glu	65	70	75
Ala Ile Leu Glu Asn Glu Asp Trp Ile Glu Asp Ala Ser Gly Leu	80	85	90
Met Ser His Cys Ile Ala Ile Leu Lys Ile Cys His Thr Leu Thr	95	100	105
Glu Lys Leu Val Ala Met Thr Met Gly Ser Gly Ala Lys Met Lys	110	115	120
Thr Ser Ala Ser Val Ser Asp Ile Ile Val Val Ala Lys Arg Ile	125	130	135
Ser Pro Arg Val Asp Asp Val Val Lys Ser Met Tyr Pro Pro Leu	140	145	150
Asp Pro Lys Leu Leu Asp Ala Arg Thr Thr Ala Leu Leu Ser	155	160	165
Val Ser His Leu Val Leu Val Thr Arg Asn Ala Cys His Leu Thr	170	175	180
Gly Gly Leu Asp Trp Ile Asp Gln Ser Leu Ser Ala Ala Glu Glu	185	190	195
His Leu Glu Val Leu Arg Glu Ala Ala Leu Ala Ser Glu Pro Asp	200	205	210
Lys Gly Leu Pro Gly Pro Glu Gly Phe Leu Gln Glu Gln Ser Ala	215	220	225
Ile			

<210> 152  
 <211> 1027  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 1017, 1020  
 <223> unknown base

<400> 152  
 gtttcatttc tcccgactca gcttccacc ctgggcttcc cgaggtgctt 50  
 tcgcgcgtgt cccaccact gcagccatga tctccttaac ggacacgcag 100  
 aaaattggaa tgggattaac aggatttga gtgtttttcc tgttctttgg 150  
 aatgattctc ttttttgaca aagcactact ggctatttga aatgttttat 200  
 ttgtagccgg cttggctttt gtaattggtt tagaagaac attcagattc 250  
 ttcttccaaa aacataaaat gaaagctaca ggtttttttc tgggtggtgt 300

attttagtgc cttattggtt ggctttgat aggcattgac ttcgaaattt 350  
 atggattttt tctcttggtc aggggcttct ttctgtgctg tgttggtttt 400  
 attagaagag tgcagtcctc tggatccctc cttaaattac ctggaattag 450  
 atcatttgta gataaagttg gagaaagcaa caatatggta taacaacaag 500  
 tgaatttgaa gactcattta aaatattgtg ttatttataa agtcatttga 550  
 agaattttca gcacaaaatt aaattacatg aaatagcttg taatgttctt 600  
 tacaggagtt taaaacgtat agcctacaaa gtaccagcag caaattagca 650  
 aagaagcagt gaaaacagcg ttctactcaa gtgaactaag aagaagtcag 700  
 caagcaaaact gagagaggtg aaatccatgt taatgatgct taagaaactc 750  
 ttgaaggcta tttgtgttgt ttttccacaa tgtgcgaaac tcagccatcc 800  
 tttagaact gtggtgcctg tttcttttct ttttattttg aaggctcagg 850  
 agcatccata ggcatttgct ttttagaagt gtccactgca atggcaaaaa 900  
 tatttccagt tgcactgtat ctctggaagt gatgcatgaa ttcgatttga 950  
 ttgtgtcatt ttaaagtatt aaaaccaagg aaaccccaat tttgatgtat 1000  
 ggattacttt tttttgngcn cagggcc 1027

<210> 153  
 <211> 138  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> N-myristoylation Sites  
 <222> 11-16, 51-56 and 116-121  
 <223> N-myristoylation Sites.

<220>  
 <221> Transmembrane domains  
 <222> 12-30, 33-52, 69-89 and 93-109  
 <223> Transmembrane domains

<220>  
 <221> Aminoacyl-transfer RNA Synthetases.  
 <222> 49-59  
 <223> Aminoacyl-transfer RNA synthetases class-II protein.

<400> 153  
 Met Ile Ser Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr  
 1 5 10 15  
 Gly Phe Gly Val Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe  
 20 25 30  
 Asp Lys Ala Leu Leu Ala Ile Gly Asn Val Leu Phe Val Ala Gly  
 35 40 45  
 Leu Ala Phe Val Ile Gly Leu Glu Arg Thr Phe Arg Phe Phe Phe  
 50 55 60



Gln Lys His Lys Met Lys Ala Thr Gly Phe Phe Leu Gly Gly Val  
65 70  
Phe Val Val Leu Ile Gly Trp Pro Leu Ile Gly Met Ile Phe Glu  
80 85 90  
Ile Tyr Gly Phe Phe Leu Leu Phe Arg Gly Phe Phe Pro Val Val  
95 100 105  
Val Gly Phe Ile Arg Arg Val Pro Val Leu Gly Ser Leu Leu Asn  
110 115 120  
Leu Pro Gly Ile Arg Ser Phe Val Asp Lys Val Gly Glu Ser Asn  
125 130 135  
Asn Met Val

<210> 154  
<211> 405  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 66  
<223> unknown base

<400> 154  
gaagacgtgg cggtctcgc ctgggctgtt tcccgcttc atttctccc 50  
actcagcttc ccacntggg ctttcgagg tgctttcgcc gctgtccca 100  
coactgcagc catgatctcc ttaacggaca cgcagaaaat tggaatggga 150  
ttaaccggat ttggagtgtt ttctctgttc ttggaatga ttctctttt 200  
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<211> 1781  
<212> DNA  
<213> Homo sapiens

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tttcttctct ctggaaatct ttgactgtgg gtagttattt atttotgaat 150  
aagagcgtcc acgcatcatg gacctcggg gactgctgaa gtctcagttc 200  
ctgtgccacc tggcttctct ctacgtcttt attgcctcag ggctaatacat 250

caacaccatt cagctcttca ctctcctcct ctggcccatt aacaagcagc 300  
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 tgtccaatt atcggctgga tgtgttactt caccgagatg gtcttctgtt 600  
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 gccatcaccg tgaggagctt gagaaatgta gtttcagctg tatatgactg 850  
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 gctgcaggg agggcagggc tggggaccga aggggacaag ttcccctttc 1650  
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 taaagtgtt tcttggttca aaaaaaaaa a 1781

<210> 156

<211> 378  
 <212> PRT  
 <213> Homo sapiens

<400> 156

Met	Asp	Leu	Ala	Gly	Leu	Leu	Lys	Ser	Gln	Phe	Leu	Cys	His	Leu	1	5	10	15
Val	Phe	Cys	Tyr	Val	Phe	Ile	Ala	Ser	Gly	Leu	Ile	Ile	Asn	Thr	20	25	30	
Ile	Gln	Leu	Phe	Thr	Leu	Leu	Leu	Trp	Pro	Ile	Asn	Lys	Gln	Leu	35	40	45	
Phe	Arg	Lys	Ile	Asn	Cys	Arg	Leu	Ser	Tyr	Cys	Ile	Ser	Ser	Gln	50	55	60	
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Gly	Thr	Glu	Cys	Thr	Ile	65	70	75	
Phe	Thr	Asp	Pro	Arg	Ala	Tyr	Leu	Lys	Tyr	Gly	Lys	Glu	Asn	Ala	80	85	90	
Ile	Val	Val	Leu	Asn	His	Lys	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly	95	100	105	
Trp	Ser	Leu	Ser	Glu	Arg	Phe	Gly	Leu	Leu	Gly	Gly	Ser	Lys	Val	110	115	120	
Leu	Ala	Lys	Lys	Glu	Leu	Ala	Tyr	Val	Pro	Ile	Ile	Gly	Trp	Met	125	130	135	
Trp	Tyr	Phe	Thr	Glu	Met	Val	Phe	Cys	Ser	Arg	Lys	Trp	Glu	Gln	140	145	150	
Asp	Arg	Lys	Thr	Val	Ala	Thr	Ser	Leu	Gln	His	Leu	Arg	Asp	Tyr	155	160	165	
Pro	Glu	Lys	Tyr	Phe	Phe	Leu	Ile	His	Cys	Glu	Gly	Thr	Arg	Phe	170	175	180	
Thr	Glu	Lys	Lys	His	Glu	Ile	Ser	Met	Gln	Val	Ala	Arg	Ala	Lys	185	190	195	
Gly	Leu	Pro	Arg	Leu	Lys	His	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly	200	205	210	
Phe	Ala	Ile	Thr	Val	Arg	Ser	Leu	Arg	Asn	Val	Val	Ser	Ala	Val	215	220	225	
Tyr	Asp	Cys	Thr	Leu	Asn	Phe	Arg	Asn	Asn	Glu	Asn	Pro	Thr	Leu	230	235	240	
Leu	Gly	Val	Leu	Asn	Gly	Lys	Lys	Tyr	His	Ala	Asp	Leu	Tyr	Val	245	250	255	
Arg	Arg	Ile	Pro	Leu	Glu	Asp	Ile	Pro	Glu	Asp	Asp	Asp	Glu	Cys	260	265	270	
Ser	Ala	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Phe	Gln	275	280	285	
Glu	Glu	Tyr	Tyr	Arg	Thr	Gly	Thr	Phe	Pro	Glu	Thr	Pro	Met	Val				

290	295	300
Pro Pro Arg Arg Pro Trp Thr Leu Val Asn Trp Leu Phe Trp Ala		
305	310	315
Ser Leu Val Leu Tyr Pro Phe Phe Gln Phe Leu Val Ser Met Ile		
320	325	330
Arg Ser Gly Ser Ser Leu Thr Leu Ala Ser Phe Ile Leu Val Phe		
335	340	345
Phe Val Ala Ser Val Gly Val Arg Trp Met Ile Gly Val Thr Glu		
350	355	360
Ile Asp Lys Gly Ser Ala Tyr Gly Asn Ser Asp Ser Lys Gln Lys		
365	370	375
Leu Asn Asp		

<210> 157  
 <211> 1849  
 <212> DNA  
 <213> Homo sapiens

<400> 157  
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 acggaaggtt ttcttcttgg ggaagtaaaa ggtgaagcca agaacagcat 150  
 tactgattcc caaatggatg atgttgaagt tgtttatata attgacattc 200  
 agaaatata tccatgctat cagcttttta gcttttataa ttcttcaggc 250  
 gaagtaaatg agcaagcact gaagaaaata ttatcaaatg tcaaaaagaa 300  
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 gacctgttt ttctgtatt aacaccaagt ataataacag aaagtgtctc 450  
 tactcatcga ctggaacatt ccttatataa acctcaaaaa ggactttttc 500  
 acagggtacc tttagtgtt gccaatctgg gcattgttga acaactgggt 550  
 tataaaactg tatcaggttc ctgtatgtcc actggtttta gccagagcag 600  
 acaaacacac agctctaaat tttttgaaga agatggatcc ttaaaggagg 650  
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 ttcatgtgtt atgtctttaa aaaatagaca tgtttctaaa agtagctgta 950

actacaacca ccatctcgat gtagtagaca atctgacctt aatggtagaa 1000  
cacactgaca ttcctgaagc tagtccagct agtacaccac aaatcattaa 1050  
gcataaaagcc ttagacttag atgacagatg gcaattcaag agatctcggt 1100  
tgttagatag acaagacaaa cgatctaaag caaatactgg tagtagtaac 1150  
caagataaag catccaaaat gagcagccca gaaacagatg aagaaattga 1200  
aaagatgaag ggttttggtg aatattcacg gtctcctaca ttttgatcct 1250  
tttaacctta caaggagatt tttttatttg gctgatgggt aagcccaaac 1300  
atttctattg tttttactat gttgagctac ttgcagtaag ttcatttgtt 1350  
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ttacttcaca aagtactttt tcaaacatca gatgctttta tttccaaacc 1450  
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tgaaaattta tctgagtcac taaaattctc cttaagtgat acttttttag 1750  
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<210> 158

<211> 409

<212> PRT

<213> Homo sapiens

<400> 158

Met	Glu	Gly	Glu	Ser	Thr	Ser	Ala	Val	Leu	Ser	Gly	Phe	Val	Leu
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Gly	Ala	Leu	Ala	Phe	Gln	His	Leu	Asn	Thr	Asp	Ser	Asp	Thr	Glu
			20						25					30
Gly	Phe	Leu	Leu	Gly	Glu	Val	Lys	Gly	Glu	Ala	Lys	Asn	Ser	Ile
			35						40					45
Thr	Asp	Ser	Gln	Met	Asp	Asp	Val	Glu	Val	Val	Tyr	Thr	Ile	Asp
			50						55					60
Ile	Gln	Lys	Tyr	Ile	Pro	Cys	Tyr	Gln	Leu	Phe	Ser	Phe	Tyr	Asn
			65						70					75
Ser	Ser	Gly	Glu	Val	Asn	Glu	Gln	Ala	Leu	Lys	Lys	Ile	Leu	Ser
			80						85					90
Asn	Val	Lys	Lys	Asn	Val	Val	Gly	Trp	Tyr	Lys	Phe	Arg	Arg	His
			95						100					105

Ser Asp Gln Ile Met Thr Phe Arg Glu Arg Leu Leu His Lys Asn  
 110 115 120  
 Leu Gln Glu His Phe Ser Asn Gln Asp Leu Val Phe Leu Leu Leu  
 125 130 135  
 Thr Pro Ser Ile Ile Thr Glu Ser Cys Ser Thr His Arg Leu Glu  
 140 145 150  
 His Ser Leu Tyr Lys Pro Gln Lys Gly Leu Phe His Arg Val Pro  
 155 160 165  
 Leu Val Val Ala Asn Leu Gly Met Ser Glu Gln Leu Gly Tyr Lys  
 170 175 180  
 Thr Val Ser Gly Ser Cys Met Ser Thr Gly Phe Ser Arg Ala Val  
 185 190 195  
 Gln Thr His Ser Ser Lys Phe Phe Glu Glu Asp Gly Ser Leu Lys  
 200 205 210  
 Glu Val His Lys Ile Asn Glu Met Tyr Ala Ser Leu Gln Glu Glu  
 215 220 225  
 Leu Lys Ser Ile Cys Lys Lys Val Glu Asp Ser Glu Gln Ala Val  
 230 235 240  
 Asp Lys Leu Val Lys Asp Val Asn Arg Leu Lys Arg Glu Ile Glu  
 245 250 255  
 Lys Arg Arg Gly Ala Gln Ile Gln Ala Ala Arg Glu Lys Asn Ile  
 260 265 270  
 Gln Lys Asp Pro Gln Glu Asn Ile Phe Leu Cys Gln Ala Leu Arg  
 275 280 285  
 Thr Phe Phe Pro Asn Ser Glu Phe Leu His Ser Cys Val Met Ser  
 290 295 300  
 Leu Lys Asn Arg His Val Ser Lys Ser Ser Cys Asn Tyr Asn His  
 305 310 315  
 His Leu Asp Val Val Asp Asn Leu Thr Leu Met Val Glu His Thr  
 320 325 330  
 Asp Ile Pro Glu Ala Ser Pro Ala Ser Thr Pro Gln Ile Ile Lys  
 335 340 345  
 His Lys Ala Leu Asp Leu Asp Asp Arg Trp Gln Phe Lys Arg Ser  
 350 355 360  
 Arg Leu Leu Asp Thr Gln Asp Lys Arg Ser Lys Ala Asn Thr Gly  
 365 370 375  
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 380 385 390  
 Asp Glu Glu Ile Glu Lys Met Lys Gly Phe Gly Glu Tyr Ser Arg  
 395 400 405  
 Ser Pro Thr Phe

<210> 159  
 <211> 2651  
 <212> DNA  
 <213> Homo sapiens

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 cgcgcgccac accctctgcg gtccccgcgg cgcctgccac ctttccctcc 150  
 ttcccccgct ccccgccctcg ccggccagtc agcttgccgg gttcgctgcc 200  
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<210> 160

<211> 556

<212> PRT

<213> Homo sapiens

<400> 160

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Leu	Ser	Ala	Ala	Leu	Leu	Ala	Ala	Glu	Leu	Lys	Ser	Lys	Ser	Cys
				20				25					30	
Ser	Glu	Val	Arg	Arg	Leu	Tyr	Val	Ser	Lys	Gly	Phe	Asn	Lys	Asn



35										40					45				
Asp	Ala	Pro	Leu	His	Glu	Ile	Asn	Gly	Asp	55	His	Leu	Lys	Ile	Cys	60			
Pro	Gln	Gly	Ser	Thr	Cys	Cys	Ser	Gln	Glu	70	Met	Glu	Glu	Lys	Tyr	75			
Ser	Leu	Gln	Ser	Lys	Asp	Asp	Phe	Lys	Ser	85	Val	Val	Ser	Glu	Gln	90			
Cys	Asn	His	Leu	Gln	Ala	Val	Phe	Ala	Ser	100	Arg	Tyr	Lys	Lys	Phe	105			
Asp	Glu	Phe	Phe	Lys	Glu	Leu	Leu	Glu	Asn	115	Ala	Glu	Lys	Ser	Leu	120			
Asn	Asp	Met	Phe	Val	Lys	Thr	Tyr	Gly	His	130	Leu	Tyr	Met	Gln	Asn	135			
Ser	Glu	Leu	Phe	Lys	Asp	Leu	Phe	Val	Glu	145	Leu	Lys	Arg	Tyr	Tyr	150			
Val	Val	Gly	Asn	Val	Asn	Leu	Glu	Glu	Met	160	Leu	Asn	Asp	Phe	Trp	165			
Ala	Arg	Leu	Leu	Glu	Arg	Met	Phe	Arg	Leu	175	Val	Asn	Ser	Gln	Tyr	180			
His	Phe	Thr	Asp	Glu	Tyr	Leu	Glu	Cys	Val	190	Ser	Lys	Tyr	Thr	Glu	195			
Gln	Leu	Lys	Pro	Phe	Gly	Asp	Val	Pro	Arg	205	Lys	Leu	Lys	Leu	Gln	210			
Val	Thr	Arg	Ala	Phe	Val	Ala	Ala	Arg	Thr	220	Phe	Ala	Gln	Gly	Leu	225			
Ala	Val	Ala	Gly	Asp	Val	Val	Ser	Lys	Val	235	Ser	Val	Val	Asn	Pro	240			
Thr	Ala	Gln	Cys	Thr	His	Ala	Leu	Leu	Lys	250	Met	Ile	Tyr	Cys	Ser	255			
His	Cys	Arg	Gly	Leu	Val	Thr	Val	Lys	Pro	265	Cys	Tyr	Asn	Tyr	Cys	270			
Ser	Asn	Ile	Met	Arg	Gly	Cys	Leu	Ala	Asn	280	Gln	Gly	Asp	Leu	Asp	285			
Phe	Glu	Trp	Asn	Asn	Phe	Ile	Asp	Ala	Met	295	Leu	Met	Val	Ala	Glu	300			
Arg	Leu	Glu	Gly	Pro	Phe	Asn	Ile	Glu	Ser	310	Val	Met	Asp	Pro	Ile	315			
Asp	Val	Lys	Ile	Ser	Asp	Ala	Ile	Met	Asn	325	Met	Gln	Asp	Asn	Ser	330			
Val	Gln	Val	Ser	Gln	Lys	Val	Phe	Gln	Gly	340	Cys	Gly	Pro	Pro	Lys	345			
Pro	Leu	Pro	Ala	Gly	Arg	Ile	Ser	Arg	Ser		Ile	Ser	Glu	Ser	Ala				

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Phe Ser Ala Arg	Phe Arg Pro His His	Pro Glu Glu Arg Pro	Thr		
	365		370		375
Thr Ala Ala Gly	Thr Ser Leu Asp Arg	Leu Val Thr Asp Val	Lys		
	380		385		390
Glu Lys Leu Lys	Gln Ala Lys Lys Phe	Trp Ser Ser Leu Pro	Ser		
	395		400		405
Asn Val Cys Asn	Asp Glu Arg Met Ala	Ala Gly Asn Gly Asn	Glu		
	410		415		420
Asp Asp Cys Trp	Asn Gly Lys Gly Lys	Ser Arg Tyr Leu Phe	Ala		
	425		430		435
Val Thr Gly Asn	Gly Leu Ala Asn Gln	Gly Asn Asn Pro Glu	Val		
	440		445		450
Gln Val Asp Thr	Ser Lys Pro Asp Ile	Leu Ile Leu Arg Gln	Ile		
	455		460		465
Met Ala Leu Arg	Val Met Thr Ser Lys	Met Lys Asn Ala Tyr	Asn		
	470		475		480
Gly Asn Asp Val	Asp Phe Phe Asp Ile	Ser Asp Glu Ser Ser	Gly		
	485		490		495
Glu Gly Ser Gly	Ser Gly Cys Glu Tyr	Gln Gln Cys Pro Ser	Glu		
	500		505		510
Phe Asp Tyr Asn	Ala Thr Asp His Ala	Gly Lys Ser Ala Asn	Glu		
	515		520		525
Lys Ala Asp Ser	Ala Gly Val Arg Pro	Gly Ala Gln Ala Tyr	Leu		
	530		535		540
Leu Thr Val Phe	Cys Ile Leu Phe Leu	Val Met Gln Arg Glu	Trp		
	545		550		555

Arg

<210> 161  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 161  
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<210> 162  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 162  
tcacatcgat gggatccatg accg 24

<210> 163  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

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<210> 164  
<211> 870  
<212> DNA  
<213> Homo sapiens

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ggaccgagcg caggcttcta ggagatggct ccagggaagg ggccaagaat 300  
gtgagtgcga agattggttc ctgagagccc cgagaagaaa attcatgaca 350  
gtgtctgggg tgccaaagaa gcagtgcctc tgtgatcatt tcaagggcaa 400  
tgtgaagaaa acaagacacc aaaggcacca cagaagacca aacaagcatt 450  
ccagagcctg ccagcaattt ctcaaacat gtcagctaa ggcctttgtc 500  
ctgcctttgt aggagctctg agcgcccaact ctccaatta aacattctca 550  
gccaaagaag cagtgcgcac acctaccaga cactcttctt ctcccacctc 600  
actctcccac tgtaccaccc cctaaatcat tcagtgctc tcaaaaagca 650  
tgtttttcaa gatcattttg tttgttgctc tctctagtgt cttcttctct 700  
cgtcagctct agcctgtgcc ctccccttac ccaggcttag gcttaattac 750  
ctgaaagatt ccaggaaact gtacgttctt agctagtgtc atttaacctt 800  
aaatgcaatc aggaaagtag caaacagaag tcaataaata tttttaaatg 850  
tcaaaaaaaaa aaaaaaaaaa 870

<210> 165  
<211> 119  
<212> PRT  
<213> Homo sapiens

<400> 165  
Met Lys Val Leu Ile Ser Ser Leu Leu Leu Leu Leu Pro Leu Met

1	5	10	15
Leu Met Ser Met Val Ser Ser Ser Leu Asn Pro Gly Val Ala Arg	20	25	30
Gly His Arg Asp Arg Gly Gln Ala Ser Arg Arg Trp Leu Gln Glu	35	40	45
Gly Gly Gln Glu Cys Glu Cys Lys Asp Trp Phe Leu Arg Ala Pro	50	55	60
Arg Arg Lys Phe Met Thr Val Ser Gly Leu Pro Lys Lys Gln Cys	65	70	75
Pro Cys Asp His Phe Lys Gly Asn Val Lys Lys Thr Arg His Gln	80	85	90
Arg His His Arg Lys Pro Asn Lys His Ser Arg Ala Cys Gln Glu	95	100	105
Phe Leu Lys Gln Cys Gln Leu Arg Ser Phe Ala Leu Pro Leu	110	115	

<210> 166  
 <211> 551  
 <212> DNA  
 <213> Homo sapiens

<400> 166  
 aatggctgtc ttagtacttc gcctgacagt tgtcctggga ctgcttgtct 50  
 tattctgtac ctgctatgca gacgacaaac cagacagacc agacgacaag 100  
 ccagacgact cgggcaaaga cccaaagcca gacttcccca aattcctaag 150  
 cctcctgggc acagagatca ttgagaatgc agtcagattc atcctccgct 200  
 ccatgtccag gagcacagga tttatggaat ttgatgataa tgaaggaaaa 250  
 cattcatcaa agtgacatcc tcaggacaca cccatgtggc tcctggacaa 300  
 tccaagagca gccaaatcct gcttttccag ttggtccca caagtctctc 350  
 aggacagagc cctcaaagca actcccaacg agttctcagg attcaggctc 400  
 tgggttcaac caaacagaac tcattttgaa caccctgact gcatttttgc 450  
 ttttagaaaag ttagaataaa tatggcgctt tgggatcaca tagttgatgg 500  
 agaggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 550  
 a 551

<210> 167  
 <211> 87  
 <212> PRT  
 <213> Homo sapiens

<400> 167  
 Met Ala Val Leu Val Leu Arg Leu Thr Val Val Leu Gly Leu Leu  
 1 5 10 15  
 Val Leu Phe Leu Thr Cys Tyr Ala Asp Asp Lys Pro Asp Lys Pro

	20		25		30
Asp Asp Lys Pro Asp Asp Ser Gly Lys Asp Pro Lys Pro Asp Phe					
	35		40		45
Pro Lys Phe Leu Ser Leu Leu Gly Thr Glu Ile Ile Glu Asn Ala					
	50		55		60
Val Glu Phe Ile Leu Arg Ser Met Ser Arg Ser Thr Gly Phe Met					
	65		70		75
Glu Phe Asp Asp Asn Glu Gly Lys His Ser Ser Lys					
	80		85		

<210> 168  
 <211> 1371  
 <212> DNA  
 <213> Homo sapiens

<400> 168  
 ggacgccagc gcctgcagag gctgagcagg gaaaagcca gtgccccagc 50  
 ggaagcacag ctccagagctg gtctgccatg gacatcctgg tccactcct 100  
 gcagctgctg gtgctgcttc ttaccctgcc cctgcacctc atggctctgc 150  
 tgggctgctg gcagccctgt tgcaaaagct acttccccta cctgatggcc 200  
 gtgtgactc ccaagagcaa ccgcaagatg gagagcaaga aacgggagct 250  
 ctccagccag ataaaggggc ttacaggagc ctccgggaaa gtggccctac 300  
 tggagctggg ctgcggaacc ggagccaact ttcatgtcta cccaccgggc 350  
 tgcagggtca cctgcctaga cccaaatccc cactttgaga agttcctgac 400  
 aaagagcatg gctgagaaca ggcacctcca atatgagcgg ttgtgtgtgg 450  
 ctctctggga ggacatgaga cagctggctg atggctccat ggatgtggtg 500  
 gtctgcactc tgggtgctgt ctctgtgcag agcccaagga aggtcctgca 550  
 ggaggtccgg agagtactga gaccgggagg tgtgctcttt ttctgggagc 600  
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 gagccacact ggaacacat tggggatggc tgctgcctca ccagagagac 700  
 ctggaaggat cttgagaacg ccagttctc cgaaatccaa atggaacgac 750  
 agcccccctc cttgaagtgg ctacctgttg ggccccacat catgggaaag 800  
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 gagggacctc gcagaatgag agaagacatt catgtaccac ctactagtcc 950  
 ctctctcccc aacctctgcc agggcaatct ctaacttcaa tcccgccttc 1000  
 gacagtgaaa aagctctact tctacgtga cccagggagg aaacactagg 1050  
 accctgttgt atctcaact gcaagtttct ggactagtct cccaacgttt 1100

gcctcccaat gttgtccctt tccttcgttc ccatggtaaa gtcctctcg 1150  
 ctttcctcct gaggtcacac ccatgcgtct ctaggaaactg gtcacaaaag 1200  
 tcatgggtgcc tgcattccctg ccaagccccc ctgaccctct ctcgccacta 1250  
 ccaccttctt cctgagctgg gggcaccagg gagaatcaga gatgctgggg 1300  
 atgccagagc aagactcaaa gaggcagagg ttttgttctc aaatattttt 1350  
 taataaatag acgaaaccac g 1371

<210> 169  
 <211> 277  
 <212> PRT  
 <213> Homo sapiens

<400> 169  
 Met Asp Ile Leu Val Pro Leu Leu Gln Leu Leu Val Leu Leu Leu  
 1 5 10 15  
 Thr Leu Pro Leu His Leu Met Ala Leu Leu Gly Cys Trp Gln Pro  
 20 25 30  
 Leu Cys Lys Ser Tyr Phe Pro Tyr Leu Met Ala Val Leu Thr Pro  
 35 40 45  
 Lys Ser Asn Arg Lys Met Glu Ser Lys Lys Arg Glu Leu Phe Ser  
 50 55 60  
 Gln Ile Lys Gly Leu Thr Gly Ala Ser Gly Lys Val Ala Leu Leu  
 65 70 75  
 Glu Leu Gly Cys Gly Thr Gly Ala Asn Phe Gln Phe Tyr Pro Pro  
 80 85 90  
 Gly Cys Arg Val Thr Cys Leu Asp Pro Asn Pro His Phe Glu Lys  
 95 100 105  
 Phe Leu Thr Lys Ser Met Ala Glu Asn Arg His Leu Gln Tyr Glu  
 110 115 120  
 Arg Phe Val Val Ala Pro Gly Glu Asp Met Arg Gln Leu Ala Asp  
 125 130 135  
 Gly Ser Met Asp Val Val Val Cys Thr Leu Val Leu Cys Ser Val  
 140 145 150  
 Gln Ser Pro Arg Lys Val Leu Gln Glu Val Arg Arg Val Leu Arg  
 155 160 165  
 Pro Gly Gly Val Leu Phe Phe Trp Glu His Val Ala Glu Pro Tyr  
 170 175 180  
 Gly Ser Trp Ala Phe Met Trp Gln Gln Val Phe Glu Pro Thr Trp  
 185 190 195  
 Lys His Ile Gly Asp Gly Cys Cys Leu Thr Arg Glu Thr Trp Lys  
 200 205 210  
 Asp Leu Glu Asn Ala Gln Phe Ser Glu Ile Gln Met Glu Arg Gln  
 215 220 225

Pro	Pro	Pro	Leu	Lys	Trp	Leu	Pro	Val	Gly	Pro	His	Ile	Met	Gly
				230					235					240
Lys	Ala	Val	Lys	Gln	Ser	Phe	Pro	Ser	Ser	Lys	Ala	Leu	Ile	Cys
				245					250					255
Ser	Phe	Pro	Ser	Leu	Gln	Leu	Glu	Gln	Ala	Thr	His	Gln	Pro	Ile
				260					265					270
Tyr	Leu	Pro	Leu	Arg	Gly	Thr								
				275										

<210> 170  
 <211> 1621  
 <212> DNA  
 <213> Homo sapiens

<400> 170  
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 cctcatcgca ggcagatgtt ggggctttgt ccgaacagct cccctctgcc 100  
 agcttctgta gataaggggtt aaaaactaat atttatatga cagaagaaaa 150  
 agatgtcatt ccgtaaagta aacatcatca tcttggtcct ggctgttgct 200  
 ctctctttac tggttttgca ccataacttc ctcagcttga gcagtttggt 250  
 aaggaatgag gttacagatt caggaattgt agggcctcaa cctatagact 300  
 ttgtccaaa tgctctocga catgcagtag atgggagaca agaggagatt 350  
 cctgtggtca tcgctgcac tgaagacagg cttggggggg ccattgcagc 400  
 tataaacagc attcagcaca acactcgctc caatgtgatt ttctacattg 450  
 ttactctcaa caatacagca gaccatctcc ggtcctggct caacagtgat 500  
 tccctgaaaa gcacagata caaaattgtc aattttgacc ctaaactttt 550  
 ggaaggaaaa gtaaaggagg atcctgacca gggggaatcc atgaacacct 600  
 taacctttgc aaggtttctac ttgccaatc tggttcccag cgcaagaag 650  
 gccatatata tggatgatga tgtaattgtg caaggtgata ttcttgccct 700  
 ttacaatata gcaactgaag caggacatgc agctgcattt toagaagatt 750  
 gtgattcagc ctctactaaa gttgtcatcc gtggagcagg aaaccagtac 800  
 aattacattg gctatcttga ctataaaaag gaaagaattc gtaagctttc 850  
 catgaaagcc agcacttgct catttaatcc tggagttttt gttgcaaacc 900  
 tgacggaatg gaaacgacag aatataacta accaactgga aaatgggatg 950  
 aaactcaatg tagaagaggg actgtatagc agaaccctgg ctggtagcat 1000  
 cacaacacct cctctgctta tcgtatttta tcaacagcac tctaccatcg 1050  
 atcctatgtg gaatgtccgc caccttggtt ccagtgtctg aaaacgatat 1100  
 tcacctcagt ttgtaaaggc tgccaagtta ctccattgga atggacattt 1150

gaagccatgg ggaaggactg cttcatatac tgatgtttgg gaaaaatggt 1200  
 atattccaga cccaacaggc aaattcaacc taatccgaag atataccgag 1250  
 atctcaaaaca taaagtgaac cagaatttga actgtaagca agcattttctc 1300  
 aggaagtccct ggaagatagc atgcatggga agtaacagtt gctaggcttc 1350  
 aatgcctatc ggtagcaagc catggaaaaa gatgtgtcag ctagggtaaag 1400  
 atgacaaact gccctgtctg gcagtcagct tccagacag actatagact 1450  
 ataaatatgt ctocatctgc cttaccaagt gttttcttac tacaatgctg 1500  
 aatgactgga aagaagaact gatatggcta gttcagctag ctggtacaga 1550  
 taattcaaaa ctgctgttgg ttttaatttt gtaacctgtg gcctgatctg 1600  
 taaataaaac ttacattttt c 1621

<210> 171  
 <211> 371  
 <212> PRT  
 <213> Homo sapiens

<400> 171  
 Met Ser Phe Arg Lys Val Asn Ile Ile Ile Leu Val Leu Ala Val  
 1 5 10 15  
 Ala Leu Phe Leu Leu Val Leu His His Asn Phe Leu Ser Leu Ser  
 20 25 30  
 Ser Leu Leu Arg Asn Glu Val Thr Asp Ser Gly Ile Val Gly Pro  
 35 40 45  
 Gln Pro Ile Asp Phe Val Pro Asn Ala Leu Arg His Ala Val Asp  
 50 55 60  
 Gly Arg Gln Glu Glu Ile Pro Val Val Ile Ala Ala Ser Glu Asp  
 65 70 75  
 Arg Leu Gly Gly Ala Ile Ala Ala Ile Asn Ser Ile Gln His Asn  
 80 85 90  
 Thr Arg Ser Asn Val Ile Phe Tyr Ile Val Thr Leu Asn Asn Thr  
 95 100 105  
 Ala Asp His Leu Arg Ser Trp Leu Asn Ser Asp Ser Leu Lys Ser  
 110 115 120  
 Ile Arg Tyr Lys Ile Val Asn Phe Asp Pro Lys Leu Leu Glu Gly  
 125 130 135  
 Lys Val Lys Glu Asp Pro Asp Gln Gly Glu Ser Met Lys Pro Leu  
 140 145 150  
 Thr Phe Ala Arg Phe Tyr Leu Pro Ile Leu Val Pro Ser Ala Lys  
 155 160 165  
 Lys Ala Ile Tyr Met Asp Asp Asp Val Ile Val Gln Gly Asp Ile  
 170 175 180  
 Leu Ala Leu Tyr Asn Thr Ala Leu Lys Pro Gly His Ala Ala Ala



	185		190		195
Phe Ser Glu Asp	Cys Asp Ser Ala Ser Thr	Lys Val Val Ile	Arg		
	200		205		210
Gly Ala Gly Asn	Gln Tyr Asn Tyr Ile	Gly Tyr Leu Asp Tyr	Lys		
	215		220		225
Lys Glu Arg Ile	Arg Lys Leu Ser Met	Lys Ala Ser Thr Cys	Ser		
	230		235		240
Phe Asn Pro Gly	Val Phe Val Ala Asn	Leu Thr Glu Trp Lys	Arg		
	245		250		255
Gln Asn Ile Thr	Asn Gln Leu Glu Lys	Trp Met Lys Leu Asn	Val		
	260		265		270
Glu Glu Gly Leu	Tyr Ser Arg Thr Leu	Ala Gly Ser Ile Thr	Thr		
	275		280		285
Pro Pro Leu Leu	Ile Val Phe Tyr Gln	Gln His Ser Thr Ile	Asp		
	290		295		300
Pro Met Trp Asn	Val Arg His Leu Gly	Ser Ser Ala Gly Lys	Arg		
	305		310		315
Tyr Ser Pro Gln	Phe Val Lys Ala Ala	Lys Leu Leu His Trp	Asn		
	320		325		330
Gly His Leu Lys	Pro Trp Gly Arg Thr	Ala Ser Tyr Thr Asp	Val		
	335		340		345
Trp Glu Lys Trp	Tyr Ile Pro Asp Pro	Thr Gly Lys Phe Asn	Leu		
	350		355		360
Ile Arg Arg Tyr	Thr Glu Ile Ser Asn	Ile Lys			
	365		370		

<210> 172

<211> 585

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 71, 76, 86, 91, 162, 220, 269, 281

<223> unknown base

<400> 172

tggtttttgc ccataaatt cctcagctt gacgagtttg ttaaggaatg 50

agggttacaga ttcaggaatt ntaggncctc aacctntaga ntttgtccca 100

aatgttctcc gacatgcagt agatgggaga caagaggaga ttctgtggt 150

catcgctgca tntgaagaca ggcttggggg ggccattgca gctataaaca 200

gcattcagca caacactcgn tccaatgtga ttttctacat tgttactctc 250

aacaatacag cagacatnt cgggtcctgg ntcaacagtg attccctgaa 300

aagcatcaga tacaaaattg tcaattttga ccctaaactt ttggaaggaa 350

aagtaaagga ggatcctgac cagggggaat ccatgaaacc tttaaccttt 400  
gcaagggtct acttgccaat tctgggtccc agcgcaaaga aggccatata 450  
catggatgat gatgtaattg tgcaagggtga tattcttgcc ctttacaata 500  
cagcactgaa gccaggacat gcagctgcat ttccagaaga ttgtgattca 550  
gcctctacta aagttgtcat ccgtggagca ggaaa 585

<210> 173  
<211> 1866  
<212> DNA  
<213> Homo sapiens

<400> 173  
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aacgcggcgc gccagacaac gggctgggct ccggggcctg cggcgcgggc 150  
gctgagctgg cagggcgggt cggggcgcgg gctgcatccg catctctccc 200  
atcgccctga gtaaggcgcg ccgcggcgag ccttgagggg gaacgacttg 250  
tcggagccct aaccaggggt gtctctgagc ctgggtggat ccccgaggag 300  
tcacatcact ttccgatcac ttcaaagtgg ttaaaaaacta atatttatat 350  
gacagaagaa aaagatgtca ttccgtaaaag taaacatcat catcttggtc 400  
ctgggctggt gctctcttct tactgggttt gcaccataac ttctcagct 450  
tgaggcagtt tgtaaggaa tgagggtaca gattcaggaa ttgtaggggc 500  
tcaacctata ggactttgtc ccaaatgctc tccgacatgc agtagatggg 550  
agacaagagg agattcctgt ggtcatcgct gcatctgaag acaggcttgg 600  
gggggccatt gcagctataa acagcattca gcacaacact cgctccaatg 650  
tgattttcta cattgttact ctcaacaata cagcagacca tctccggtcc 700  
tgggctcaac agtgattccc tgaaaagcat cagatataaa attgtcaatt 750  
ttgaccotaa acttttgtaa ggaaaagtaa aggaggatcc tgaccagggg 800  
gaatccatga aacctttaac ctttgcaagg ttctacttgc caattctggg 850  
ttccacgccc aaagaaggcc atatacatgg atgatgatgt aatttgcaa 900  
ggtgatatto ttgcccttta caatacagca ctgaagccag gacatgcagc 950  
tgcattttca gaagattgtg attcagccctc tactaaagtt gtcacccgtg 1000  
gagcaggaaa ccagtacaat tacattggct atcttgacta taaaagggaa 1050  
agaattcgta agctttccat gaaagccagc acttgctcat ttaatcctgg 1100  
agtttttgtt gcaaacctga cggaatggaa acgacagaat ataactaacc 1150  
aactggaaaa atggatgaaa ctcaatgtag aagagggact gtatagcaga 1200

accctggctg gtagcatcac aacacctcct ctgcttatcg tattttatca 1250  
 acagcactct accatcgatc ctatgtggaa tgtccgccac cttggttcca 1300  
 gtgtcggaaa acgatattca cctcagtttg taaaggctgc caagtactc 1350  
 cattggaatg gacatttgaa gccatgggga aggactgctt catatactga 1400  
 tgtttgggga aaaatgggat attccagacc caacaggcaa attcaaccta 1450  
 atccgaagat ataccgagat ctcaaacata aagtgaacaa gaatttgaac 1500  
 tgtaagcaag catttctcag gaagtctcgg aagatagcat gcgtgggaag 1550  
 taacagttgc taggcttcaa tgcctatcgg tagcaagcca tggaaaaaga 1600  
 tgtgtcagct aggtaaagat gacaaactgc cctgtctggc agtcagcttc 1650  
 ccagacagac tatagactat aaatatgtct ccactctgct taccaagtgt 1700  
 tttcttacta caatgctgaa tgactggaaa gaagaactga tatggctagt 1750  
 tcagctagct ggtacagata attcaaaact gctgttggtt ttaattttgt 1800  
 aacctgtggc ctgatctgta aataaaactt acatttttca ataggtaaaa 1850  
 aaaaaaaaaa aaaaaa 1866

<210> 174  
 <211> 823  
 <212> DNA  
 <213> Homo sapiens

<400> 174  
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 ctcaccattg aggcagctcc actgtctgtg ctggtctgag ggtgctgcct 150  
 gtcattgggg cagccatctc ccagggggcc ctcatcgcca tcgtctgcaa 200  
 cggctctctg ggcttcttgc tgctgctgct ctgggtcctc ctctgctggg 250  
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 agccatgaag gcagctacct gctgcagccc tgaaggcccc tggcctagcc 400  
 tggagccag gacctaaagt cacctcacct agagcctgga attaggatcc 450  
 cagagttcag ccagcctggg gtccagaact caagagtcog cctgcttga 500  
 gctggaccca gcggcccaga gtctagccag cttggctcca ataggagctc 550  
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 gaggccaggg catctggact atgctccatc ccaagggccca agggctcagg 650  
 gccgggtcca ctctttccct aggctgagca cctctaggcc ctctaggttg 700  
 ggggaagcaa ctggaaccga tggcaataat aggagggtgt ccaggctggg 750

ccccccccc ggctcccca gtgtttgctg gataataaat ggaactatgg 800

ctctaaaaaa aaaaaaaaaa aaa 823

<210> 175

<211> 87

<212> PRT

<213> Homo sapiens

<400> 175

Met Gly Ala Ala Ile Ser Gln Gly Ala Leu Ile Ala Ile Val Cys  
1 5 10 15

Asn Gly Leu Val Gly Phe Leu Leu Leu Leu Trp Val Ile Leu  
20 25 30

Cys Trp Ala Cys His Ser Arg Leu Pro Thr Leu Thr Leu Ser Leu  
35 40 45

Asn Pro Val Pro Thr Pro Ala Leu Ala Pro Val Leu Arg Arg Pro  
50 55 60

His His Pro Arg Ser Pro Ala Met Lys Ala Ala Thr Cys Cys Ser  
65 70 75

Pro Glu Gly Pro Trp Pro Ser Leu Glu Pro Arg Thr  
80 85

<210> 176

<211> 1660

<212> DNA

<213> Homo sapiens

<400> 176

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cccaggctac cagttcctcc aagcaagtca ttcccttat ttaaccgatg 100

tgtccctcaa acacctgagt gctactccct atttgcatct gttttgataa 150

atgatgttga caccctccac cgaattctaa gtggaatcat gtcgggaaga 200

gataacaatcc ttggcctgtg tatcctcgca tttagcctgt ctttgcccat 250

gatgtttacc ttcagattca tcaccacctc tctggttcac attttcattt 300

cattggttat tttgggattg ttgtttgtct gcggtgtttt atggtggctg 350

tattatgact ataccaacga cctcagcata gaattggaca cagaaaggga 400

aaatatgaag tgcgtgctgg ggtttgctat cgtatccaca ggcacacagg 450

cagtgcgtct cgtcttgatt tttgtttcca gaaagagaat aaaattgaca 500

gttgagcttt tccaaatcac aaataaagcc atcagcagtg ctoccttcct 550

gctgttccag ccaactgtga catttgccat cctcatttcc ttctgggtcc 600

tctgggtggc tgtgctgctg agcctgggaa ctgcaggagc tgcccagggt 650

atggaaggcg gccaaagtga atataagccc ctttcgggca ttcggtacat 700

gtggctgtac catttaattg gcctcatctg gactagttaa ttcattcttg 750

cgtgccagca aatgactata gctggggcag tggttacttg ttatttcaac 800  
 agaagtaaaa atgatcctcc tgatcatccc atcctttcgt ctctctccat 850  
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 ctgctgtttc tgggtgcttg acaaatacct gctccatctc aaccagaatg 1050  
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 gatgcattca aaatcttgto caagaactca agtcacttta catctattaa 1150  
 ctgctttgga gacttcataa tttttctagg aaaggtgtta gtggtgtgtt 1200  
 tcaactgttt tggaggactc atggctttta actacaatcg ggcattccag 1250  
 gtgtgggcag tccctctgtt attggtagct tttttgcct acttagtagc 1300  
 ccatagtttt ttatctgtgt ttgaaactgt gctggatgca cttttcctgt 1350  
 gttttgtctg tgatctggaa acaaatgatg gatcgtcaga aaagccctac 1400  
 tttatggatc aagaatttct gagtctcgta aaaaggagca acaaatataa 1450  
 caatgcaagg gcacagcagg acaagcactc attaaggaat gaggagggaa 1500  
 cagaactcca ggccattgtg agatagatac ccatttaggt atctgtacct 1550  
 ggaaaacatt tccttctaag agccatttac agaatagaag atgagaccac 1600  
 tagagaaaag ttagtgaatt tttttttaa agacctaata aaccctattc 1650  
 ttcctcaaaa 1660

<210> 177  
 <211> 445  
 <212> PRT  
 <213> Homo sapiens

<400> 177  
 Met Ser Gly Arg Asp Thr Ile Leu Gly Leu Cys Ile Leu Ala Leu  
 1 5 10 15  
 Ala Leu Ser Leu Ala Met Met Phe Thr Phe Arg Phe Ile Thr Thr  
 20 25 30  
 Leu Leu Val His Ile Phe Ile Ser Leu Val Ile Leu Gly Leu Leu  
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 Phe Val Cys Gly Val Leu Trp Trp Leu Tyr Tyr Asp Tyr Thr Asn  
 50 55 60  
 Asp Leu Ser Ile Glu Leu Asp Thr Glu Arg Glu Asn Met Lys Cys  
 65 70 75  
 Val Leu Gly Phe Ala Ile Val Ser Thr Gly Ile Thr Ala Val Leu  
 80 85 90  
 Leu Val Leu Ile Phe Val Leu Arg Lys Arg Ile Lys Leu Thr Val

	95	100	105
Glu Leu Phe Gln Ile Thr Asn Lys Ala	110	Ile Ser Ser Ala Pro	Phe 120
Leu Leu Phe Gln Pro Leu Trp Thr Phe	125	Ala Ile Leu Ile Phe	Phe 135
Trp Val Leu Trp Val Ala Val Leu Leu	140	Ser Leu Gly Thr Ala	Gly 150
Ala Ala Gln Val Met Glu Gly Gly Gln	155	Val Glu Tyr Lys Pro	Leu 165
Ser Gly Ile Arg Tyr Met Trp Ser Tyr	170	His Leu Ile Gly Leu	Ile 180
Trp Thr Ser Glu Phe Ile Leu Ala Cys	185	Gln Gln Met Thr Ile	Ala 195
Gly Ala Val Val Thr Cys Tyr Phe Asn	200	Arg Ser Lys Asn Asp	Pro 210
Pro Asp His Pro Ile Leu Ser Ser Leu	215	Ser Ile Leu Phe Phe	Tyr 225
His Gln Gly Thr Val Val Lys Gly Ser	230	Phe Leu Ile Ser Val	Val 240
Arg Ile Pro Arg Ile Ile Val Met Tyr	245	Met Gln Asn Ala Leu	Lys 255
Glu Gln Gln His Gly Ala Leu Ser Arg	260	Tyr Leu Phe Arg Cys	Cys 270
Tyr Cys Cys Phe Trp Cys Leu Asp Lys	275	Tyr Leu Leu His Leu	Asn 285
Gln Asn Ala Tyr Thr Thr Thr Ala Ile	290	Asn Gly Thr Asp Phe	Cys 300
Thr Ser Ala Lys Asp Ala Phe Lys Ile	305	Leu Ser Lys Asn Ser	Ser 315
His Phe Thr Ser Ile Asn Cys Phe Gly	320	Asp Phe Ile Ile Phe	Leu 330
Gly Lys Val Leu Val Val Cys Phe Thr	335	Val Phe Gly Gly Leu	Met 345
Ala Phe Asn Tyr Asn Arg Ala Phe Gln	350	Val Trp Ala Val Pro	Leu 360
Leu Leu Val Ala Phe Phe Ala Tyr Leu	365	Val Ala His Ser Phe	Leu 375
Ser Val Phe Glu Thr Val Leu Asp Ala	380	Leu Phe Leu Cys Phe	Ala 390
Val Asp Leu Glu Thr Asn Asp Gly Ser	395	Ser Glu Lys Pro Tyr	Phe 405
Met Asp Gln Glu Phe Leu Ser Phe Val		Lys Arg Ser Asn Lys	Leu

410

415

420

Asn Asn Ala Arg Ala Gln Gln Asp Lys His Ser Leu Arg Asn Glu  
425 430 435

Glu Gly Thr Glu Leu Gln Ala Ile Val Arg  
440 445

&lt;210&gt; 178

&lt;211&gt; 2773

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 178

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<211> 678  
 <212> PRT  
 <213> Homo sapiens

<400> 179

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Ala	Lys	Lys	Ile	Lys	Arg	Pro	Lys	Phe	Thr	Val	Pro	Gln	Ile	Asn	
			35						40					45	
Cys	Asp	Val	Lys	Ala	Gly	Lys	Ile	Ile	Asp	Pro	Glu	Phe	Ile	Val	
			50						55					60	
Lys	Cys	Pro	Ala	Gly	Cys	Gln	Asp	Pro	Lys	Tyr	His	Val	Tyr	Gly	
			65						70					75	
Thr	Asp	Val	Tyr	Ala	Ser	Tyr	Ser	Ser	Val	Cys	Gly	Ala	Ala	Val	
				80					85					90	
His	Ser	Gly	Val	Leu	Asp	Asn	Ser	Gly	Gly	Lys	Ile	Leu	Val	Arg	
				95					100					105	
Lys	Val	Ala	Gly	Gln	Ser	Gly	Tyr	Lys	Gly	Ser	Tyr	Ser	Asn	Gly	
			110						115					120	
Val	Gln	Ser	Leu	Ser	Leu	Pro	Arg	Trp	Arg	Glu	Ser	Phe	Ile	Val	
			125						130					135	
Leu	Glu	Ser	Lys	Pro	Lys	Lys	Gly	Val	Thr	Tyr	Pro	Ser	Ala	Leu	
			140						145					150	
Thr	Tyr	Ser	Ser	Ser	Lys	Ser	Pro	Ala	Ala	Gln	Ala	Gly	Glu	Thr	
			155						160					165	
Thr	Lys	Ala	Tyr	Gln	Arg	Pro	Pro	Ile	Pro	Gly	Thr	Thr	Ala	Gln	
			170						175					180	
Pro	Val	Thr	Leu	Met	Gln	Leu	Leu	Ala	Val	Thr	Val	Ala	Val	Ala	
			185						190					195	
Thr	Pro	Thr	Thr	Leu	Pro	Arg	Pro	Ser	Pro	Ser	Ala	Ala	Ser	Thr	
			200						205					210	
Thr	Ser	Ile	Pro	Arg	Pro	Gln	Ser	Val	Gly	His	Arg	Ser	Gln	Glu	
			215						220					225	
Met	Asp	Leu	Trp	Ser	Thr	Ala	Thr	Tyr	Thr	Ser	Ser	Gln	Asn	Arg	
			230						235					240	
Pro	Arg	Ala	Asp	Pro	Gly	Ile	Gln	Arg	Gln	Asp	Pro	Ser	Gly	Ala	
			245						250					255	
Ala	Phe	Gln	Lys	Pro	Val	Gly	Ala	Asp	Val	Ser	Leu	Gly	Leu	Val	
			260						265					270	
Pro	Lys	Glu	Glu	Leu	Ser	Thr	Gln	Ser	Leu	Glu	Pro	Val	Ser	Leu	
			275						280					285	
Gly	Asp	Pro	Asn	Cys	Lys	Ile	Asp	Leu	Ser	Phe	Leu	Ile	Asp	Gly	

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				305					310					315					
Leu	Ala	Asp	Val	Ala	Gln	Ala	Leu	Asp	Ile	Gly	Pro	Ala	Gly	Pro					
				320					325					330					
Leu	Met	Gly	Val	Val	Gln	Tyr	Gly	Asp	Asn	Pro	Ala	Thr	His	Phe					
				335					340					345					
Asn	Leu	Lys	Thr	His	Thr	Asn	Ser	Arg	Asp	Leu	Lys	Thr	Ala	Ile					
				350					355					360					
Glu	Lys	Ile	Thr	Gln	Arg	Gly	Gly	Leu	Ser	Asn	Val	Gly	Arg	Ala					
				365					370					375					
Ile	Ser	Phe	Val	Thr	Lys	Asn	Phe	Phe	Ser	Lys	Ala	Asn	Gly	Asn					
				380					385					390					
Arg	Ser	Gly	Ala	Pro	Asn	Val	Val	Val	Val	Met	Val	Asp	Gly	Trp					
				395					400					405					
Pro	Thr	Asp	Lys	Val	Glu	Glu	Ala	Ser	Arg	Leu	Ala	Arg	Glu	Ser					
				410					415					420					
Gly	Ile	Asn	Ile	Phe	Phe	Ile	Thr	Ile	Glu	Gly	Ala	Ala	Glu	Asn					
				425					430					435					
Glu	Lys	Gln	Tyr	Val	Val	Glu	Pro	Asn	Phe	Ala	Asn	Lys	Ala	Val					
				440					445					450					
Cys	Arg	Thr	Asn	Gly	Phe	Tyr	Ser	Leu	His	Val	Gln	Ser	Trp	Phe					
				455					460					465					
Gly	Leu	His	Lys	Thr	Leu	Gln	Pro	Leu	Val	Lys	Arg	Val	Cys	Asp					
				470					475					480					
Thr	Asp	Arg	Leu	Ala	Cys	Ser	Lys	Thr	Cys	Leu	Asn	Ser	Ala	Asp					
				485					490					495					
Ile	Gly	Phe	Val	Ile	Asp	Gly	Ser	Ser	Ser	Val	Gly	Thr	Gly	Asn					
				500					505					510					
Phe	Arg	Thr	Val	Leu	Gln	Phe	Val	Thr	Asn	Leu	Thr	Lys	Glu	Phe					
				515					520					525					
Glu	Ile	Ser	Asp	Thr	Asp	Thr	Arg	Ile	Gly	Ala	Val	Gln	Tyr	Thr					
				530					535					540					
Tyr	Glu	Gln	Arg	Leu	Glu	Phe	Gly	Phe	Asp	Lys	Tyr	Ser	Ser	Lys					
				545					550					555					
Pro	Asp	Ile	Leu	Asn	Ala	Ile	Lys	Arg	Val	Gly	Tyr	Trp	Ser	Gly					
				560					565					570					
Gly	Thr	Ser	Thr	Gly	Ala	Ala	Ile	Asn	Phe	Ala	Leu	Glu	Gln	Leu					
				575					580					585					
Phe	Lys	Lys	Ser	Lys	Pro	Asn	Lys	Arg	Lys	Leu	Met	Ile	Leu	Ile					
				590					595					600					
Thr	Asp	Gly	Arg	Ser	Tyr	Asp	Asp	Val	Arg	Ile	Pro	Ala	Met	Ala					

605	610	615
Ala His Leu Lys Gly Val Ile Thr Tyr	Ala Ile Gly Val Ala Trp	
620	625	630
Ala Ala Gln Glu Glu Leu Glu Val Ile	Ala Thr His Pro Ala Arg	
635	640	645
Asp His Ser Phe Phe Val Asp Glu Phe	Asp Asn Leu His Gln Tyr	
650	655	660
Val Pro Arg Ile Ile Gln Asn Ile Cys	Thr Glu Phe Asn Ser Gln	
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Pro Arg Asn

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 <211> 1759  
 <212> DNA  
 <213> Homo sapiens

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<210> 181  
<211> 541  
<212> PRT  
<213> Homo sapiens

<400> 181  
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Asp Pro Ala His Tyr Ser Phe Ser Leu Thr Leu Ile Asp Ala Leu  
35 40 45  
Asp Thr Leu Leu Ile Leu Gly Asn Val Ser Glu Phe Gln Arg Val  
50 55 60  
Val Glu Val Leu Gln Asp Ser Val Asp Phe Asp Ile Asp Val Asn  
65 70 75  
Ala Ser Val Phe Glu Thr Asn Ile Arg Val Val Gly Gly Leu Leu  
80 85 90  
Ser Ala His Leu Leu Ser Lys Lys Ala Gly Val Glu Val Glu Ala  
95 100 105  
Gly Trp Pro Cys Ser Gly Pro Leu Leu Arg Met Ala Glu Glu Ala  
110 115 120  
Ala Arg Lys Leu Leu Pro Ala Phe Gln Thr Pro Thr Gly Met Pro

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Tyr Gly Thr Val	Asn Leu Leu His Gly	Val Asn Pro Gly Glu Thr			
	140	145			150
Pro Val Thr Cys	Thr Ala Gly Ile Gly Thr	Phe Ile Val Glu Phe			
	155	160			165
Ala Thr Leu Ser	Ser Leu Thr Gly Asp Pro	Val Phe Glu Asp Val			
	170	175			180
Ala Arg Val Ala	Leu Met Arg Leu Trp Glu	Ser Arg Ser Asp Ile			
	185	190			195
Gly Leu Val Gly	Asn His Ile Asp Val	Leu Thr Gly Lys Trp Val			
	200	205			210
Ala Gln Asp Ala	Gly Ile Gly Ala Gly	Val Asp Ser Tyr Phe Glu			
	215	220			225
Tyr Leu Val Lys	Gly Ala Ile Leu Leu Gln	Asp Lys Lys Leu Met			
	230	235			240
Ala Met Phe Leu	Glu Tyr Asn Lys Ala Ile	Arg Asn Tyr Thr Arg			
	245	250			255
Phe Asp Asp Trp	Tyr Leu Trp Val Gln Met	Tyr Lys Gly Thr Val			
	260	265			270
Ser Met Pro Val	Phe Gln Ser Leu Glu Ala	Tyr Trp Pro Gly Leu			
	275	280			285
Gln Ser Leu Ile	Gly Asp Ile Asp Asn Ala	Met Arg Thr Phe Leu			
	290	295			300
Asn Tyr Tyr Thr	Val Trp Lys Gln Phe Gly	Gly Leu Pro Glu Phe			
	305	310			315
Tyr Asn Ile Pro	Gln Gly Tyr Thr Val Glu	Lys Arg Glu Gly Tyr			
	320	325			330
Pro Leu Arg Pro	Glu Leu Ile Glu Ser Ala	Met Tyr Leu Tyr Arg			
	335	340			345
Ala Thr Gly Asp	Pro Thr Leu Leu Glu Leu	Gly Arg Asp Ala Val			
	350	355			360
Glu Ser Ile Glu	Lys Ile Ser Lys Val Glu	Cys Gly Phe Ala Thr			
	365	370			375
Ile Lys Asp Leu	Arg Asp His Lys Leu Asp	Asn Arg Met Glu Ser			
	380	385			390
Phe Phe Leu Ala	Glu Thr Val Lys Tyr Leu	Tyr Leu Leu Phe Asp			
	395	400			405
Pro Thr Asn Phe	Ile His Asn Asn Gly Ser	Thr Phe Asp Ala Val			
	410	415			420
Ile Thr Pro Tyr	Gly Glu Cys Ile Leu Gly	Ala Gly Gly Tyr Ile			
	425	430			435
Phe Asn Thr Glu	Ala His Pro Ile Asp Leu	Ala Ala Leu His Cys			

440	445	450
Cys Gln Arg Leu Lys Glu Glu Gln Trp Glu Val Glu Asp Leu Met		
455	460	465
Arg Glu Phe Tyr Ser Leu Lys Arg Ser Arg Ser Lys Phe Gln Lys		
470	475	480
Asn Thr Val Ser Ser Gly Pro Trp Glu Pro Pro Ala Arg Pro Gly		
485	490	495
Thr Leu Phe Ser Pro Glu Asn His Asp Gln Ala Arg Glu Arg Lys		
500	505	510
Pro Ala Lys Gln Lys Val Pro Leu Leu Ser Cys Pro Ser Gln Pro		
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Phe Thr Ser Lys Leu Ala Leu Leu Gly Gln Val Phe Leu Asp Ser		
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Ser

<210> 182  
 <211> 2056  
 <212> DNA  
 <213> Homo sapiens

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 tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200  
 gctttatttt ggaagaaac aatgttctag gtcaaaactga gtctaccaa 250  
 tgcagacttt cacaatggtt ctagaagaaa tctggacaag tcttttcatg 300  
 tggtttttct acgcattgat tccatgtttg ctcacagatg aagtggccat 350  
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 acctggttat tgagctggag gacctggggc ccaggtttga gttcctgtg 750  
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 tgactgattc agtgtttctg gagagcagga cataaatgta tgatgagaat 1650  
 gatcaaggac tctacacact ggggtgcttg gagagcccac tttccagaa 1700  
 taatccttga gagaaaagga atcatgggag caatgggtgt gagttcactt 1750  
 caagcccaat gccgggtgcag agggggaatg cttagcgcgc tctacagtag 1800  
 gtgacctgga ggaaggtcac agccacactg aaaatgggat gtgcataaac 1850  
 acggaggatc catgaactac tgtaaagtgt tgacagtgtg tgcacactgc 1900  
 agacagcagg tgaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950  
 gtaacatgtg catgtttgtt gtgtccttt tttctgttg taaagtacag 2000  
 aattcagcaa ataaaaagg ccaccctggc caaaagcggg aaaaaaaaaa 2050  
 aaaaaa 2056

<210> 183  
 <211> 311  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> Signal peptide  
 <222> 1-29  
 <223> Signal peptide

<220>  
 <221> N-glycosylation sites  
 <222> 40-43, 134-137

<223> N-glycosylation sites.

<220>

<221> Tissue factor proteins homology

<222> 92-119

<223> Tissue factor proteins homology

<220>

<221> Transmembrane domain

<222> 230-255

<223> Transmembrane domain

<220>

<221> Integrins alpha chain protein homology

<222> 232-262

<223> Integrins alpha chain protein homology

<400> 183

Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu  
1 5 10 15

Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp  
20 25 30

Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser  
35 40 45

Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro  
50 55 60

Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu  
65 70 75

Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser  
80 85 90

Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala  
95 100 105

Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln  
110 115 120

Thr Ser Ala Trp Ser Ile Leu Lys His Pro Phe Asn Arg Asn Ser  
125 130 135

Thr Ile Leu Thr Arg Pro Gly Met Glu Ile Thr Lys Asp Gly Phe  
140 145 150

His Leu Val Ile Glu Leu Glu Asp Leu Gly Pro Gln Phe Glu Phe  
155 160 165

Leu Val Ala Tyr Trp Arg Arg Glu Pro Gly Ala Glu Glu His Val  
170 175 180

Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu Glu Thr Met  
185 190 195

Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe Val Lys  
200 205 210

Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val Glu  
215 220 225



Val	Gln	Gly	Glu	Ala	Ile	Pro	Leu	Val	Leu	Ala	Leu	Phe	Ala	Phe	
				230					235					240	
Val	Gly	Phe	Met	Leu	Ile	Leu	Val	Val	Val	Pro	Leu	Phe	Val	Trp	
				245					250					255	
Lys	Met	Gly	Arg	Leu	Leu	Gln	Tyr	Ser	Cys	Cys	Pro	Val	Val	Val	
				260					265					270	
Leu	Pro	Asp	Thr	Leu	Lys	Ile	Thr	Asn	Ser	Pro	Gln	Lys	Leu	Ile	
				275					280					285	
Ser	Cys	Arg	Arg	Glu	Glu	Val	Asp	Ala	Cys	Ala	Thr	Ala	Val	Met	
				290					295					300	
Ser	Pro	Glu	Glu	Leu	Leu	Arg	Ala	Trp	Ile	Ser					
				305					310						

<210> 184  
 <211> 808  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 654, 711, 748  
 <223> unknown base

<400> 184  
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 tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150  
 agaatgcttt attttggaaa gaaacaatgt tctagggtcaa actgagtcta 200  
 ccaaatgcag actttcacia tggttctaga agaaatctgg acaagtcttt 250  
 tcatgtgtgt tttctacgca ttgattccat gtttgctcac agatgaagtg 300  
 gccattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350  
 gcctctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400  
 attctgtcga ataccagggg gagtacgaga gcctgtacac gagccacatc 450  
 tggatcccca gcagctggtg ctcaactcact gaaggctcct agtgtgatgt 500  
 cactgatgac atcacggcca ctgtgccata caacctttgt gtcaggggcca 550  
 catttgggtc acagacctca gcctggagca tcttgaagca tccctttaat 600  
 agaaactcaa ccatccttac ccgacctggg atggagatca ccaaagatgg 650  
 cttncacctg gttattgagc tggaggacot ggggccccag tttaggttcc 700  
 ttgtggccta ntggaggagg ggcgaaacccc ttgcggcgca aggggttngc 750  
 gaaccccttg cgccgctgg ggtatctctc gagaaaagag aggcccaata 800  
 tgacccac 808

<210> 185  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 185  
aggcttcgct gcgactagac ctc 23

<210> 186  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 186  
ccaggtcggg taaggatggt tgag 24

<210> 187  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 187  
tttctaagca ttgattccat gtttctcac agatgaagt gccattctgc 50

<210> 188  
<211> 1227  
<212> DNA  
<213> Homo sapiens

<400> 188  
cggaacgctg ggccgccacc tccggaacaa gccatggtgg cggcgacggt 50  
ggcagcggcg tggctgctcc tgtgggctgc ggctgcgcg cagcaggagc 100  
aggacttcta cgacttcaag gcggtcaaca tccggggcaa actggtgtcg 150  
ctggagaagt accgcggatc ggtgtccctg gtggtgaatg tggccagcga 200  
gtgcggcttc acagaccagc actaccgagc cctgcagcag ctgcagcgag 250  
acctggggccc ccaccacttt aacgtgctcg ccttcccctg caaccagttt 300  
ggccaacagg agcctgacag caacaaggag attgagagct ttgccgcgcg 350  
cacctacagt gtctcattcc ccatgtttag caagattgca gtcaccggta 400  
ctggtgccca tcttccttcc aagtacctgg ccagacttcc tgggaaggag 450  
cccacctgga acttctggaa gtacctagta gcccagatg gaaaggtggt 500  
aggggcttgg gacccaactg tgcagtggga ggaggtcaga cccagatca 550  
cagcgctcgt gaggaagctc atcctactga agcgagaaga cttataacca 600

ccgcgtctcc tctccacca cctcatcccg cccacctgtg tggggctgac 650  
 caatgcaaac tcaaatgggtg cttcaaaggg agagaccac tgactctcct 700  
 tcctttactc ttatgccatt ggtccatca ttctgtggg ggaataatc 750  
 tagtattttg attatttgaa tcttacagca acaaatagga actcctggcc 800  
 aatgagagct cttgaccagt gaatcaccag ccgatacgaa cgtcttgcca 850  
 acaaaaatgt gtggcaata gaagtatatc aagcaataat cccccacca 900  
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 attaggatga aatacctgtg aaagtgccta ggcagtgcc gcaaatagg 1000  
 aggcattcaa tgaacatttt ttgcataaa accaaaaaat aactgtttat 1050  
 caataaaaaa ttgcatccaa catgaatttc cagccgatga taatccaggc 1100  
 caaagggtta gttgttgta tttcctctgt attattttct tcattacaaa 1150  
 agaaatgcaa gttcattgta acaatccaaa caatacctca cgatataaaa 1200  
 taaaaatgaa agtatcctcc tcaaaaa 1227

<210> 189

<211> 187

<212> PRT

<213> Homo sapiens

<400> 189

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Ala	Ala	Cys	Ala	Gln	Gln	Glu	Gln	Asp	Phe	Tyr	Asp	Phe	Lys	Ala
			20					25						30
Val	Asn	Ile	Arg	Gly	Lys	Leu	Val	Ser	Leu	Glu	Lys	Tyr	Arg	Gly
			35					40						45
Ser	Val	Ser	Leu	Val	Val	Asn	Val	Ala	Ser	Glu	Cys	Gly	Phe	Thr
			50					55						60
Asp	Gln	His	Tyr	Arg	Ala	Leu	Gln	Gln	Leu	Gln	Arg	Asp	Leu	Gly
			65					70						75
Pro	His	His	Phe	Asn	Val	Leu	Ala	Phe	Pro	Cys	Asn	Gln	Phe	Gly
			80					85						90
Gln	Gln	Glu	Pro	Asp	Ser	Asn	Lys	Glu	Ile	Glu	Ser	Phe	Ala	Arg
			95					100						105
Arg	Thr	Tyr	Ser	Val	Ser	Phe	Pro	Met	Phe	Ser	Lys	Ile	Ala	Val
			110					115						120
Thr	Gly	Thr	Gly	Ala	His	Pro	Ala	Phe	Lys	Tyr	Leu	Ala	Gln	Thr
			125					130						135
Ser	Gly	Lys	Glu	Pro	Thr	Trp	Asn	Phe	Trp	Lys	Tyr	Leu	Val	Ala
			140					145						150
Pro	Asp	Gly	Lys	Val	Val	Gly	Ala	Trp	Asp	Pro	Thr	Val	Ser	Val

155 160 165  
 Glu Glu Val Arg Pro Gln Ile Thr Ala Leu Val Arg Lys Leu Ile  
 170 175 180  
 Leu Leu Lys Arg Glu Asp Leu  
 185

<210> 190  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 190  
 gcaggacttc tacgacttca aggc 24

<210> 191  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 191  
 agtctgggcc aggtacttga aggc 24

<210> 192  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 192  
 caacatccgg ggcaaacctgg tgcgctgga gaagtaccgc ggatcgggtg 50

<210> 193  
 <211> 2187  
 <212> DNA  
 <213> Homo sapiens

<400> 193  
 cggacgcgtg ggcggggccgg gacgcaggcc aaagcgagcc atggctgtct 50  
 acgtcgggat gctgcgcctg gggaggctgt gcgccgggag ctcgggggtg 100  
 ctggggggccc gggccgccct ctctcggagt tggcaggaag ccaggttgca 150  
 ggggtgtccgc ttctcagtt ccagagaggt ggatcgcgat gtctccacgc 200  
 ccatcggagg cctcagctac gttcaggggg gcaccaaaaa gcatcttaac 250  
 agcaagactg tgggccagtg cctggagacc acagcacaga gggctcccaga 300  
 acgagaggcc ttggtcgtcc tccatgaaga cgtcagggtg acctttgcc 350  
 aactcaagga ggaggtggac aaagctgctt ctggcctcct gacgattggc 400

ctctgcaaa gtagccggct gggcatgtgg ggacctaact cctatgcatg 450  
 ggtgtctcatg cagttggcca ccgcccaggc gggcatcatt ctggtgtctg 500  
 tgaaccacgc ctaccagget atggaactgg agtatgtcct caagaagggtg 550  
 ggctgcaagg cccttgtgtt ccccaagcaa ttcaagacct agcaatacta 600  
 caacgtcctg aagcagatct gtccagaagt ggagaatgcc cagccagggg 650  
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 cacacggcag catctggacc agctccaata caaccagcag ttctgtcct 800  
 gccatgacct catcaacatc cagttcacct cggggacaac aggcagcccc 850  
 aagggggcca ccctctocca ctacaacatt gtcaacaact ccaacatttt 900  
 aggagagcgc ctgaaactgc atgagaagac accagagcag ttgcggatga 950  
 tcttgcccaa cccctgtac cattgcctgg gttccgtggc aggcacaatg 1000  
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 atggtacccc cacgatgttc gtggacattc tgaaccagcc agacttctcc 1150  
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 gtttgtcaca aactaccccc tcaccatttc aggaagatc cagaaattca 1850  
 aacttcgaga gcagatggaa cgacatctaa atctgtgaat aaagcagcag 1900  
 gcctgtcctg gccggttgcc ttgaatctct cctgtcagaa tgcaacctgg 1950  
 ctttatgcac ctatgatgtc ccagacccca gttctgagcc aggcacatca 2000

aatgtcaagg aattgactga acgaactaag agctcctgga tgggtccggg 2050  
aactgcctg ggcacaaggt gccaaaaggc aggcagcctg cccaggccct 2100  
ccctcctgtc catccccac attccctgt ctgtcctgt gatttggcat 2150  
aaagagcttc tgttttctt gaaaaaaaa aaaaaaa 2187

<210> 194  
<211> 615  
<212> PRT  
<213> Homo sapiens

<400> 194  
Met Ala Val Tyr Val Gly Met Leu Arg Leu Gly Arg Leu Cys Ala  
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Gly Ser Ser Gly Val Leu Gly Ala Arg Ala Ala Leu Ser Arg Ser  
20 25 30  
Trp Gln Glu Ala Arg Leu Gln Gly Val Arg Phe Leu Ser Ser Arg  
35 40 45  
Glu Val Asp Arg Met Val Ser Thr Pro Ile Gly Gly Leu Ser Tyr  
50 55 60  
Val Gln Gly Cys Thr Lys Lys His Leu Asn Ser Lys Thr Val Gly  
65 70 75  
Gln Cys Leu Glu Thr Thr Ala Gln Arg Val Pro Glu Arg Glu Ala  
80 85 90  
Leu Val Val Leu His Glu Asp Val Arg Leu Thr Phe Ala Gln Leu  
95 100 105  
Lys Glu Glu Val Asp Lys Ala Ala Ser Gly Leu Leu Ser Ile Gly  
110 115 120  
Leu Cys Lys Gly Asp Arg Leu Gly Met Trp Gly Pro Asn Ser Trp  
125 130 135  
Ala Trp Val Leu Met Gln Leu Ala Thr Ala Gln Ala Gly Ile Ile  
140 145 150  
Leu Val Ser Val Asn Pro Ala Tyr Gln Ala Met Glu Leu Glu Tyr  
155 160 165  
Val Leu Lys Lys Val Gly Cys Lys Ala Leu Val Phe Pro Lys Gln  
170 175 180  
Phe Lys Thr Gln Gln Tyr Tyr Asn Val Leu Lys Gln Ile Cys Pro  
185 190 195  
Glu Val Glu Asn Ala Gln Pro Gly Ala Leu Lys Ser Gln Arg Leu  
200 205 210  
Pro Asp Leu Thr Thr Val Ile Ser Val Asp Ala Pro Leu Pro Gly  
215 220 225  
Thr Leu Leu Leu Asp Glu Val Val Ala Ala Gly Ser Thr Arg Gln  
230 235 240  
His Leu Asp Gln Leu Gln Tyr Asn Gln Gln Phe Leu Ser Cys His

245	250	255
Asp Pro Ile Asn Ile Gln Phe Thr Ser Gly Thr Thr Gly Ser Pro		
260	265	270
Lys Gly Ala Thr Leu Ser His Tyr Asn Ile Val Asn Asn Ser Asn		
275	280	285
Ile Leu Gly Glu Arg Leu Lys Leu His Glu Lys Thr Pro Glu Gln		
290	295	300
Leu Arg Met Ile Leu Pro Asn Pro Leu Tyr His Cys Leu Gly Ser		
305	310	315
Val Ala Gly Thr Met Met Cys Leu Met Tyr Gly Ala Thr Leu Ile		
320	325	330
Leu Ala Ser Pro Ile Phe Asn Gly Lys Lys Ala Leu Glu Ala Ile		
335	340	345
Ser Arg Glu Arg Gly Thr Phe Leu Tyr Gly Thr Pro Thr Met Phe		
350	355	360
Val Asp Ile Leu Asn Gln Pro Asp Phe Ser Ser Tyr Asp Ile Ser		
365	370	375
Thr Met Cys Gly Gly Val Ile Ala Gly Ser Pro Ala Pro Pro Glu		
380	385	390
Leu Ile Arg Ala Ile Ile Asn Lys Ile Asn Met Lys Asp Leu Val		
395	400	405
Val Ala Tyr Gly Thr Thr Glu Asn Ser Pro Val Thr Phe Ala His		
410	415	420
Phe Pro Glu Asp Thr Val Glu Gln Lys Ala Glu Ser Val Gly Arg		
425	430	435
Ile Met Pro His Thr Glu Ala Arg Ile Met Asn Met Glu Ala Gly		
440	445	450
Thr Leu Ala Lys Leu Asn Thr Pro Gly Glu Leu Cys Ile Arg Gly		
455	460	465
Tyr Cys Val Met Leu Gly Tyr Trp Gly Glu Pro Gln Lys Thr Glu		
470	475	480
Glu Ala Val Asp Gln Asp Lys Trp Tyr Trp Thr Gly Asp Val Ala		
485	490	495
Thr Met Asn Glu Gln Gly Phe Cys Lys Ile Val Gly Arg Ser Lys		
500	505	510
Asp Met Ile Ile Arg Gly Gly Glu Asn Ile Tyr Pro Ala Glu Leu		
515	520	525
Glu Asp Phe Phe His Thr His Pro Lys Val Gln Glu Val Gln Val		
530	535	540
Val Gly Val Lys Asp Asp Arg Met Gly Glu Glu Ile Cys Ala Cys		
545	550	555
Ile Arg Leu Lys Asp Gly Glu Glu Thr Thr Val Glu Glu Ile Lys		

560	565	570
Ala Phe Cys Lys Gly Lys Ile Ser His Phe Lys Ile Pro Lys Tyr		
575	580	585
Ile Val Phe Val Thr Asn Tyr Pro Leu Thr Ile Ser Gly Lys Ile		
590	595	600
Gln Lys Phe Lys Leu Arg Glu Gln Met Glu Arg His Leu Asn Leu		
605	610	615

<210> 195  
 <211> 642  
 <212> DNA  
 <213> Homo sapiens

<400> 195  
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 gtggcaggca caatgatgtg tctgatgtac ggtgccccc tcatcctggc 150  
 ctctcccac ttcaatggca agaaggcact ggaggccatc agcagagaga 200  
 gaggcacctt cctgtatggt acccccacga tgtctgtgga cattctgaac 250  
 cagccagact tctccagtta tgacatctcg accatgtgtg gaggtgtcat 300  
 tgctgggtcc cctgcacctc cagagttgat ccgagccatc atcaacaaga 350  
 taaatatgaa ggacctggtg gttgcttatg gaaccacaga gaacagtccc 400  
 gtgacattcg cgcacttccc tgaggacact gtggagcaga aggcagaaag 450  
 cgtgggcaga attatgcctc acacggaggc gcggtatcat aacatggagg 500  
 cagggacgct ggcaaagctg aacacgcccg gggagctgtg catccgaggg 550  
 tactgcgtca tgctgggcta ctggggtgag cctcagaaga cagaggaagc 600  
 agtggatcag gacaagtggg attggacagg agatgtcgcc ac 642

<210> 196  
 <211> 1575  
 <212> DNA  
 <213> Homo sapiens

<400> 196  
 gagcaggagc gagccatgga ccccgccagg aaagcagggtg ccaggcccat 50  
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 agggccctgga gtgctacagc tcgtgcgaga aagcagatga cggatgctcc 150  
 ccgaacaaga tgaagacagt gaagtgcgcg ccgggctgtg acgtctgcac 200  
 cgaggccgtg ggggcgggtg agaccatcca cggacaattc tcgtggcag 250  
 tgcgggggtg cggttcggga ctcccggca agaatgaccg cggtctggat 300  
 cttaacgggc ttctgctgtt catccagctg cagcaatgag ctcaggatcg 350



ctgcaacgcc aagctcaacc tcacctcgcg ggcgctcgac ccggcaggta 400  
 atgagagtgc ataccgcccc aacggcgctgg agtgctacag ctgtgtgggc 450  
 ctgagccggg aggcgtgccca gggtagcatcg ccgccggtcg tagctgcta 500  
 caacgccagc gatcatgtct acaagggctg ctctgacggc aacgtcacct 550  
 tgacggcagc taatgtgact gtgtccttgc ctgtccgggg ctgtgtccag 600  
 gatgaattct gcaactggga tggagtaaca ggcccagggt tcacgctcag 650  
 tggctcctgt tgccaggggt ccgctgttaa ctctgacctc cgcaacaaga 700  
 cctactcttc cctcgaatc ccaccccttg tccggtgcgc cctccagag 750  
 cccacgactg tggcctcaac cacatctgtc accacttcta cctcgcccc 800  
 agtgagaccc acatccacca ccaaacccat gccagcgcca accagtcaga 850  
 ctccgagaca gggagtagaa cagcaggcct ccggggatga ggagcccagg 900  
 ttgactggag gcgcgctgg ccaccaggac cgcagcaatt cagggcagta 950  
 tctgcaaaa ggggggcccc agcagcccca taataaaggc tgtgtggctc 1000  
 ccacagctgg attggcagcc cttctgttgg ccgtggctgc tgggttccta 1050  
 ctgtgagctt ctccacctgg aaatttccct ctccactact tctctggccc 1100  
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 gccagcccc tgtttttcca acattcccca gtatccccag cttctgctgc 1200  
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 ggggtttcta gctttttgag gacagctcct gtatccttct catccttgtc 1300  
 tctccgcttg tctcttctgt atgttaggac agagtgcagc aagtcagctg 1350  
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 tagccagcct ggactttgga gcgtgggggtg ggtggggcaa tggctcccca 1450  
 ctctaagcac tgccctccct actcccgcca tctttgggga atcggttccc 1500  
 catatgtctt ccttactaga ctgtgagctc ctccaggggg ggcccggtag 1550  
 ccaattcgcc ctatagtgcg tcgta 1575

<210> 197

<211> 346

<212> PRT

<213> Homo sapiens

<400> 197

Met Asp Pro Ala Arg Lys Ala Gly Ala Gln Ala Met Ile Trp Thr  
           1                          5                          10                          15

Ala Gly Trp Leu Leu Leu Leu Leu Arg Gly Gly Ala Gln Ala  
                           20                          25                          30

Leu Glu Cys Tyr Ser Cys Val Gln Lys Ala Asp Asp Gly Cys Ser

	35	40	45
Pro Asn Lys Met	Lys Thr Val Lys Cys	Ala	Pro Gly Val Asp Val
	50	55	60
Cys Thr Glu Ala	Val Gly Ala Val Glu Thr	Ile His Gly Gln Phe	
	65	70	75
Ser Leu Ala Val Arg	Gly Cys Gly Ser Gly	Leu Pro Gly Lys Asn	
	80	85	90
Asp Arg Gly Leu	Asp Leu His Gly Leu	Leu Ala Phe Ile Gln Leu	
	95	100	105
Gln Gln Cys Ala	Gln Asp Arg Cys Asn Ala	Lys Leu Asn Leu Thr	
	110	115	120
Ser Arg Ala Leu	Asp Pro Ala Gly Asn Glu	Ser Ala Tyr Pro Pro	
	125	130	135
Asn Gly Val Glu	Cys Tyr Ser Cys Val Gly	Leu Ser Arg Glu Ala	
	140	145	150
Cys Gln Gly Thr	Ser Pro Pro Val Val	Ser Cys Tyr Asn Ala Ser	
	155	160	165
Asp His Val Tyr	Lys Gly Cys Phe Asp	Gly Asn Val Thr Leu Thr	
	170	175	180
Ala Ala Asn Val	Thr Val Ser Leu Pro	Val Arg Gly Cys Val Gln	
	185	190	195
Asp Glu Phe Cys	Thr Arg Asp Gly Val	Thr Gly Pro Gly Phe Thr	
	200	205	210
Leu Ser Gly Ser	Cys Cys Gln Gly Ser	Arg Cys Asn Ser Asp Leu	
	215	220	225
Arg Asn Lys Thr	Tyr Phe Ser Pro Arg	Ile Pro Pro Leu Val Arg	
	230	235	240
Leu Pro Pro Pro	Glu Pro Thr Thr Val	Ala Ser Thr Thr Ser Val	
	245	250	255
Thr Thr Ser Thr	Ser Ala Pro Val Arg	Pro Thr Ser Thr Thr Lys	
	260	265	270
Pro Met Pro Ala	Pro Thr Ser Gln Thr	Pro Arg Gln Gly Val Glu	
	275	280	285
His Glu Ala Ser	Arg Asp Glu Glu Pro	Leu Thr Gly Gly Ala	
	290	295	300
Ala Gly His Gln	Asp Arg Ser Asn Ser	Gly Gln Tyr Pro Ala Lys	
	305	310	315
Gly Gly Pro Gln	Gln Pro His Asn Lys	Gly Cys Val Ala Pro Thr	
	320	325	330
Ala Gly Leu Ala	Ala Leu Leu Leu Ala	Val Ala Ala Gly Val Leu	
	335	340	345

Leu

<210> 198  
 <211> 1657  
 <212> DNA  
 <213> Homo sapiens

<400> 198  
 cgggactcgg cgggtcctcc tgggagtctc ggaggggacc ggctgtgcag 50  
 acgccatgga gttggtgctg gtcttcctct gcagcctgct ggccccatg 100  
 gtccctggcca gtgcagctga aaaggagaag gaaatggacc cttttcatta 150  
 tgattaccag accctgagga ttgggggact ggtgttcgct gtggtcctct 200  
 tctcggttgg gatcctcctt atcctaagtc gcaggtgcaa gtgcagtttc 250  
 aatcagaagc cccgggcccc aggagatgag gaagcccagg tggagaacct 300  
 catcacccgc aatgcaacag agccccagaa gcagagaact gaagtgcagc 350  
 catcagggtg aagcctctgg aacctgaggc ggctgcttga acctttggat 400  
 gcaaattgtc atgcttaaga aaaccggcca cttcagcaac agccctttcc 450  
 ccaggagaag ccaagaactt gtgtgtcccc caccctatcc cctctaacac 500  
 cattctcca cctgatgatg caactaacac ttgcctcccc actgcagcct 550  
 gcggtcctgc ccacctcccg tgatgtgtgt gtgtgtgtgt gtgtgtgact 600  
 gtgtgtgttt gctaactgtg gtctttgtgg ctaactgttt gtggatggta 650  
 ttgtgtttgt tagtgaactg tggactcgct ttcccaggca ggggctgagc 700  
 cacatggcca tctgctctc cctgcccccg tggccctcca tcacctctg 750  
 ctctaggag gctgcttgtt gcccgagacc agccccctcc cctgatttag 800  
 ggatgcgtag ggttaagagca cgggcagtgg tcttcagtcg tcttgggacc 850  
 tgggaaggtt tgcagcactt tgtcatcatt cttcatggac tcctttcact 900  
 cctttaacaa aaaccttgct tccttatccc acctgatccc agtctgaagg 950  
 tctcttagca actggagata caaagcaagg agctggtagag ccagcgttg 1000  
 acgtcaggca ggctatgccc ttccgtggtt aatttcttcc caggggcttc 1050  
 cacgaggagt ccccatctgc ccgccccctt cacagagcgc cgggggatc 1100  
 caggcccagg gcttctaact tgcacctggg gaatgtgtcc cctgcatac 1150  
 ttctcagcaa taactccatg ggctctggga cctaccocct tccaaccttc 1200  
 cctgcttctg agacttcaat ctacagccca gctcatccag atgcagacta 1250  
 cagtcocctg aattgggtct ctggcaggca atagttgaag gactcctgtt 1300  
 ccgttggggc cagcacaccg ggatggatgg agggagagca gaggcctttg 1350  
 cttctctgcc tacgtcccct tagatgggca gcagaggcaa ctccgcgcatc 1400

ctttgctctg cctgtcgggtg gtcagagcgg tgagcgaggt ggggttgaga 1450  
ctcagcaggc tccgtgcagc ccttggaac agtgagaggt tgaaggatcat 1500  
aacgagagtg ggaactcaac ccagatcccg cccctcctgt cctctgtgtt 1550  
cccgcggaac ccaaccaaac cgtgcgctgt gacccattgc tgttctctgt 1600  
atcgtgatct atcctcaaca acaacagaaa aaaggaataa aatatccttt 1650  
gtttct 1657

<210> 199  
<211> 120  
<212> PRT  
<213> Homo sapiens

<400> 199  
Met Glu Leu Val Leu Val Phe Leu Cys Ser Leu Leu Ala Pro Met  
1 5 10 15  
Val Leu Ala Ser Ala Ala Glu Lys Glu Lys Glu Met Asp Pro Phe  
20 25 30  
His Tyr Asp Tyr Gln Thr Leu Arg Ile Gly Gly Leu Val Phe Ala  
35 40 45  
Val Val Leu Phe Ser Val Gly Ile Leu Leu Ile Leu Ser Arg Arg  
50 55 60  
Cys Lys Cys Ser Phe Asn Gln Lys Pro Arg Ala Pro Gly Asp Glu  
65 70 75  
Glu Ala Gln Val Glu Asn Leu Ile Thr Ala Asn Ala Thr Glu Pro  
80 85 90  
Gln Lys Gln Arg Thr Glu Val Gln Pro Ser Gly Gly Ser Leu Trp  
95 100 105  
Asn Leu Arg Arg Leu Leu Glu Pro Leu Asp Ala Asn Val Asp Ala  
110 115 120

<210> 200  
<211> 415  
<212> DNA  
<213> Homo sapiens

<400> 200  
aaacttgacg ccattgaagat cccggtcctt cctgccgttg tgctcctctc 50  
cctcctggtg ctccactctg ccaggggagc caccctgggt ggtcctgagg 100  
aagaagacac cattgagaat tatgcgtcac gaccggaggc cttaaacacc 150  
cgttctctga acatcgacaa attgcgatct gcgtttaagg ctgatgagtt 200  
cctgaacttg cagccctct ttgagtctat caaaaggaaa ctctctttcc 250  
tcaactggga tgcctttcct aagctgaaag gactgaggag cgcaactcct 300  
gatgccagc gaccatgacc tccactggaa gagggggcta gcgtgagcgc 350  
tgattctcaa cctaccataa ctctttctct cctcaggaac tccaataaaa 400

cattttccat ccaaa 415

<210> 201

<211> 99

<212> PRT

<213> Homo sapiens

<400> 201

Met	Lys	Ile	Pro	Val	Leu	Pro	Ala	Val	Val	Leu	Leu	Ser	Leu	Leu
1				5					10					15
Val	Leu	His	Ser	Ala	Gln	Gly	Ala	Thr	Leu	Gly	Gly	Pro	Glu	Glu
			20						25					30
Glu	Ser	Thr	Ile	Glu	Asn	Tyr	Ala	Ser	Arg	Pro	Glu	Ala	Phe	Asn
			35						40					45
Thr	Pro	Phe	Leu	Asn	Ile	Asp	Lys	Leu	Arg	Ser	Ala	Phe	Lys	Ala
			50						55					60
Asp	Glu	Phe	Leu	Asn	Trp	His	Ala	Leu	Phe	Glu	Ser	Ile	Lys	Arg
			65						70					75
Lys	Leu	Pro	Phe	Leu	Asn	Trp	Asp	Ala	Phe	Pro	Lys	Leu	Lys	Gly
			80						85					90
Leu	Arg	Ser	Ala	Thr	Pro	Asp	Ala	Gln						
				95										

<210> 202

<211> 678

<212> DNA

<213> Homo sapiens

<400> 202

cagttctgaa atcaatggag ttaatttagg gaatacaaac cagccatggg 50  
ggtggagatt gcttttgct cagtgattct cacctgcctc tcccttctgg 100  
cagcaggagt ctcccagggt gttctctccc agccagttcc aactcaggag 150  
acagggtccca aggccatggg agatctctcc tgtggctttg cgggccactc 200  
atgagagtgt ttttgtgtaa agtatttttt agaatactgt tgacttcttc 250  
atgatttaat aaccatcctt tgcgaagttt tatgaggctt taggggaatg 300  
tcaaccctca aatttttggt atactagatg gcttccattt acccaccact 350  
attttaaggt ccttttattt ttaggttcaa gggttcattg acttgagaaa 400  
gtgcctctct gcagcttcat tgattttggt tatcttctact attaatgta 450  
acgattaaaa aagaataaga gcacgcagac ctctaggaga atattttatc 500  
cctgggtgcc cctgacacat ttatgtagt atccacaaa tgtgattggt 550  
aatttaaatg ttatttctaatt attagtacat tcagttgtga tgtaatatga 600  
ataaccagaa totatttctt aaaagttttg agtatatttt tcaactagat 650  
atttgatatg aaagactgaa tagtgatg 678

<210> 203  
 <211> 52  
 <212> PRT  
 <213> Homo sapiens

<400> 203  
 Met Gly Val Glu Ile Ala Phe Ala Ser Val Ile Leu Thr Cys Leu  
 1 5 10 15  
 Ser Leu Leu Ala Ala Gly Val Ser Gln Val Val Leu Leu Gln Pro  
 20 25 30  
 Val Pro Thr Gln Glu Thr Gly Pro Lys Ala Met Gly Asp Leu Ser  
 35 40 45  
 Cys Gly Phe Ala Gly His Ser  
 50

<210> 204  
 <211> 1917  
 <212> DNA  
 <213> Homo sapiens

<400> 204  
 ggggaactctg cagtaggtct gccggcgcgatg gagtgggtggg ctagctcgcc 50  
 gcttcggctc tggtgctgt tgttctctct gccctcagcg cagggccgcc 100  
 agaaggagtc aggttcaaaa tggaaagtat ttattgacca aattaacagg 150  
 tctttggaga attacgaacc atgttcaagt caaaactgca gctgctacca 200  
 tgggtgtcata gaagaggato taactccttt ccgaggaggc atctccagga 250  
 agatgatggc agaggtagtc agacgggaagc tagggaccga ctatcagatc 300  
 actaagaaca gactgtaccg ggaaaatgac tgcatgttcc cctcaagggtg 350  
 tagtggtgtt gagcacttta ttttggaaag gatcggggcgt ctccctgaca 400  
 tggagatggt gatcaatgta cgagattatc ctcagggttcc taaatggatg 450  
 gagcctgccca tccagctctt ctcttcagtc aagacatcag agtaccatga 500  
 tatcatgtat cctgcttgga catttttgga agggggacct gctgtttggc 550  
 caatttatcc tacagggtctt ggacgggtggg acctcttcag agaagatctg 600  
 gtaagggtcag cagcacagtg gccatggaaa aagaaaaact ctacagcata 650  
 ttcccgagga tcaaggacaa gtccagaacg agatcctctc attcttctgt 700  
 ctccgaaaaa cccaaaactt gttgatgcag aatacaccaa aaaccaggcc 750  
 tggaaatcta tgaagatac cttaggaaag ccagctgtcta aggatgtcca 800  
 tcttgtggat cactgcaaat acaagtatct gtttaatttt cgaggcgtag 850  
 ctgcaagttt ccggtttaa cactctcttc tgtgtggctc actgttttcc 900  
 catgttggtg atgagtggct agaattcttc tatccacagc tgaagccatg 950  
 ggttcacat atcccagtc aaacagatct ctccaatgct caagagctgt 1000

tacaatttgt aaaagcaaat gatgatgtag ctcaagagat tgctgaaagg 1050  
 ggaagccagt ttattaggaa ccatttgagc atggatgaca tcacctgtta 1100  
 ctgggagaaac ctcttgagtg aataactctaa attcctgtct tataatgtaa 1150  
 cgagaaggaa aggttatgat caaattattc ccaaaatggt gaaaactgaa 1200  
 ctatagtagt catcatagga ccatagtctt ctttgtggca acagatctca 1250  
 gatatcctac ggtgagaagc ttaccataag cttggtcctt atacctgaa 1300  
 tatctgctat caagccaaat acctgggttt ccttatcatg ctgcaccag 1350  
 agcaactctt gagaaagatt taaaatgtgt ctaatacaact gatatgaagc 1400  
 agttcaactt tttggatgaa taaggaccag aaactgtgag atgtggattt 1450  
 tgaacccaac tctaccttct attttcttaa gaccaatcac agcttgtgcc 1500  
 tcagatcctc cacctgtgtg agtccatcac tgtgaaattg actgtgtcca 1550  
 tgtgatgatg ccctttgtcc cattatttgg agcagaaaaat tcgtcatttg 1600  
 gaagtagtac aactcattgc tggaaattgtg aaattattca aggcgtgatc 1650  
 tctgtcactt tattttaatg taggaaaccc tatgggggtt atgaaaaata 1700  
 cttggggatc attctctgaa tggctctaagg aagcggtagc catgccatgc 1750  
 aatgatgtag gagttctctt ttgtaaaacc ataaactctg ttactcagga 1800  
 ggtttctata atgccacata gaaagaggcc aattgcata gtaattattg 1850  
 caattggatt tcagggtccc tttttgtgcc ttcatgccct acttcttaat 1900  
 gcctctctaa agccaaa 1917

<210> 205  
 <211> 392  
 <212> PRT  
 <213> Homo sapiens

<400> 205  
 Met Glu Trp Trp Ala Ser Ser Pro Leu Arg Leu Trp Leu Leu Leu  
 1 5 10 15  
 Phe Leu Leu Pro Ser Ala Gln Gly Arg Gln Lys Glu Ser Gly Ser  
 20 25 30  
 Lys Trp Lys Val Phe Ile Asp Gln Ile Asn Arg Ser Leu Glu Asn  
 35 40 45  
 Tyr Glu Pro Cys Ser Ser Gln Asn Cys Ser Cys Tyr His Gly Val  
 50 55 60  
 Ile Glu Glu Asp Leu Thr Pro Phe Arg Gly Gly Ile Ser Arg Lys  
 65 70 75  
 Met Met Ala Glu Val Val Arg Arg Lys Leu Gly Thr His Tyr Gln  
 80 85 90  
 Ile Thr Lys Asn Arg Leu Tyr Arg Glu Asn Asp Cys Met Phe Pro

95					100					105				
Ser	Arg	Cys	Ser	Gly	Val	Glu	His	Phe	Ile	Leu	Glu	Val	Ile	Gly
				110					115					120
Arg	Leu	Pro	Asp	Met	Glu	Met	Val	Ile	Asn	Val	Arg	Asp	Tyr	Pro
				125					130					135
Gln	Val	Pro	Lys	Trp	Met	Glu	Pro	Ala	Ile	Pro	Val	Phe	Ser	Phe
				140					145					150
Ser	Lys	Thr	Ser	Glu	Tyr	His	Asp	Ile	Met	Tyr	Pro	Ala	Trp	Thr
				155					160					165
Phe	Trp	Glu	Gly	Gly	Pro	Ala	Val	Trp	Pro	Ile	Tyr	Pro	Thr	Gly
				170					175					180
Leu	Gly	Arg	Trp	Asp	Leu	Phe	Arg	Glu	Asp	Leu	Val	Arg	Ser	Ala
				185					190					195
Ala	Gln	Trp	Pro	Trp	Lys	Lys	Lys	Asn	Ser	Thr	Ala	Tyr	Phe	Arg
				200					205					210
Gly	Ser	Arg	Thr	Ser	Pro	Glu	Arg	Asp	Pro	Leu	Ile	Leu	Leu	Ser
				215					220					225
Arg	Lys	Asn	Pro	Lys	Leu	Val	Asp	Ala	Glu	Tyr	Thr	Lys	Asn	Gln
				230					235					240
Ala	Trp	Lys	Ser	Met	Lys	Asp	Thr	Leu	Gly	Lys	Pro	Ala	Ala	Lys
				245					250					255
Asp	Val	His	Leu	Val	Asp	His	Cys	Lys	Tyr	Lys	Tyr	Leu	Phe	Asn
				260					265					270
Phe	Arg	Gly	Val	Ala	Ala	Ser	Phe	Arg	Phe	Lys	His	Leu	Phe	Leu
				275					280					285
Cys	Gly	Ser	Leu	Val	Phe	His	Val	Gly	Asp	Glu	Trp	Leu	Glu	Phe
				290					295					300
Phe	Tyr	Pro	Gln	Leu	Lys	Pro	Trp	Val	His	Tyr	Ile	Pro	Val	Lys
				305					310					315
Thr	Asp	Leu	Ser	Asn	Val	Gln	Glu	Leu	Leu	Gln	Phe	Val	Lys	Ala
				320					325					330
Asn	Asp	Asp	Val	Ala	Gln	Glu	Ile	Ala	Glu	Arg	Gly	Ser	Gln	Phe
				335					340					345
Ile	Arg	Asn	His	Leu	Gln	Met	Asp	Asp	Ile	Thr	Cys	Tyr	Trp	Glu
				350					355					360
Asn	Leu	Leu	Ser	Glu	Tyr	Ser	Lys	Phe	Leu	Ser	Tyr	Asn	Val	Thr
				365					370					375
Arg	Arg	Lys	Gly	Tyr	Asp	Gln	Ile	Ile	Pro	Lys	Met	Leu	Lys	Thr
				380					385					390
Glu	Leu													

<210> 206



<211> 1425  
 <212> DNA  
 <213> Homo sapiens

<400> 206  
 caccctccca tttctcgcca tggccctgc actgctctg atccctgctg 50  
 ccctcgctc tttcatcctg gcctttggca ccggagtggg gttegtgcgc 100  
 tttacctccc ttggccact tcttgaggg atcccgagt ctggtggctc 150  
 ggatgccgc cagggatggc tggtgccct gcaggaccgc agcatcctg 200  
 cccctctggc atgggatctg gggctcctgc tctatttgt tgggcagcac 250  
 agcctcatg cagctgaaag agtgaaggca tggacatccc ggtactttgg 300  
 ggtccttcag aggtcactgt atgtggcctg cactgccctg gccttgccgc 350  
 tgggtgatgc gtactgggag ccataccca aaggccctgt gttgtgggag 400  
 gctcgggctg agccatgggc cactgggtg ccgctcctct gctttgtgct 450  
 ccatgtcatc tcttgctcc tcatctttag catccttctc gtctttgact 500  
 atgctgagct catgggcctc aaacagggtat actaccatgt gctggggctg 550  
 ggcgagcctc tggccctgaa gtctcccggt gctctcagac tcttctccca 600  
 cctgcgccac ccagtgtgtg tggagctgct gacagtgtg tgggtgggtg 650  
 ctaccttggt caccgaccgt ctctccttg ctttctcct tacctctac 700  
 ctgggcctgg ctacgggctg tgatcagcaa gacctccgt acctccggg 750  
 ccagctacaa agaaaactcc acctgctctc tcggcccag gatggggagg 800  
 cagagtggg agctcactct ggttaacaag cctgttcttc ctctccact 850  
 gaattctaaa tcttaacat ccaggccctg gctgcttcat gccagaggcc 900  
 caaatccatg gactgaagga gatgccctt ctactacttg agactttatt 950  
 ctctgggtcc agctccatac cctaaattct gagtttcagc cactgaactc 1000  
 caaggtccac ttctcaccag caaggaagag tggggatagg aagtcactg 1050  
 tcccttcaat gtttagagca tgacactctc cccctcaaca gcctcctgag 1100  
 aaggaaggga tctgccctga ccactccctt ggcactgtta cttgcctctg 1150  
 cgcctcaggg gtcccttctt gcaccgtgg cttccactcc aagaagggtg 1200  
 accagggtct gcaagttaaa cggctatagc tgtccctcca ggcccaacc 1250  
 ttgcctcacc actccgggcc ctagtctctg cactcctta ggccctgcct 1300  
 ctgggctcag accccaacct agtcaagggg attctcctgc tcttaactcg 1350  
 atgacttggg gctccctgct ctcccgagga agatgctctg caggaaaata 1400  
 aaagtcagcc tttttctaaa aaaa 1425

<210> 207  
 <211> 262  
 <212> PRT  
 <213> Homo sapiens

<400> 207  
 Met Ala Pro Ala Leu Leu Leu Ile Pro Ala Ala Leu Ala Ser Phe  
 1 5 10 15  
 Ile Leu Ala Phe Gly Thr Gly Val Glu Phe Val Arg Phe Thr Ser  
 20 25 30  
 Leu Arg Pro Leu Leu Gly Gly Ile Pro Glu Ser Gly Gly Pro Asp  
 35 40 45  
 Ala Arg Gln Gly Trp Leu Ala Ala Leu Gln Asp Arg Ser Ile Leu  
 50 55 60  
 Ala Pro Leu Ala Trp Asp Leu Gly Leu Leu Leu Phe Val Gly  
 65 70 75  
 Gln His Ser Leu Met Ala Ala Glu Arg Val Lys Ala Trp Thr Ser  
 80 85 90  
 Arg Tyr Phe Gly Val Leu Gln Arg Ser Leu Tyr Val Ala Cys Thr  
 95 100 105  
 Ala Leu Ala Leu Gln Leu Val Met Arg Tyr Trp Glu Pro Ile Pro  
 110 115 120  
 Lys Gly Pro Val Leu Trp Glu Ala Arg Ala Glu Pro Trp Ala Thr  
 125 130 135  
 Trp Val Pro Leu Leu Cys Phe Val Leu His Val Ile Ser Trp Leu  
 140 145 150  
 Leu Ile Phe Ser Ile Leu Leu Val Phe Asp Tyr Ala Glu Leu Met  
 155 160 165  
 Gly Leu Lys Gln Val Tyr Tyr His Val Leu Gly Leu Gly Glu Pro  
 170 175 180  
 Leu Ala Leu Lys Ser Pro Arg Ala Leu Arg Leu Phe Ser His Leu  
 185 190 195  
 Arg His Pro Val Cys Val Glu Leu Leu Thr Val Leu Trp Val Val  
 200 205 210  
 Pro Thr Leu Gly Thr Asp Arg Leu Leu Leu Ala Phe Leu Leu Thr  
 215 220 225  
 Leu Tyr Leu Gly Leu Ala His Gly Leu Asp Gln Gln Asp Leu Arg  
 230 235 240  
 Tyr Leu Arg Ala Gln Leu Gln Arg Lys Leu His Leu Leu Ser Arg  
 245 250 255  
 Pro Gln Asp Gly Glu Ala Glu  
 260

<210> 208  
 <211> 2095  
 <212> DNA

<213> Homo sapiens

<400> 208  
ccgagcacag gagattgcct gcgttttagga ggtggctgcg ttgtgggaaa 50  
agctatcaag gaagaaattg ccaaaccatg tcttttttct tgttttcaga 100  
gtagttcaca acagatctga gtgttttaat taagcatgga atacagaaaa 150  
caacaaaaaa cttaagcttt aatttcattc tgaattccac agttttctta 200  
gtccctcgga ccgggttgac ctgttggtgc tcccgcgtgg ctgctctatc 250  
acgtggtgct ctccgactac tcaccccgag tgtaagaagc cttcggctcg 300  
cgtgcttctg agctgctgtg gatggcctcg gctctctgga ctgtccttcc 350  
gagtaggatg tcaactgagat cctcacaatg gaggctcctg ctgctgtcac 400  
tcctgagttt ctttgtgatg tggtaacctc gccctcccca ctacaatgtg 450  
atagaacgcg tgaactggat gtacttctat gagtatgagc cgattttacag 500  
acaagacttt cacttcacac ttcgagagca ttcaaaactgc tctcatcaaa 550  
atccatttct ggtoattctg gtgacctccc acccttcaga tgtgaaagcc 600  
aggcaggcca ttagagttac ttggggtgaa aaaaagctct ggtggggata 650  
tgagggttctt acatttttct tattaggcca agaggctgaa aaggaagaca 700  
aaatgttggc attgtcctta gaggatgaac accttcttta tgggtgacata 750  
atcgacaaag attttttaga cacatataat aacctgacct tgaaaacccat 800  
tatggcattc aggtgggtaa ctgagttttg cccaatgcc aagtacgtaa 850  
tgaagacaga cactgatgtt ttcataata ctggcaattt agtgaagtat 900  
cttttaaacc taaaccactc agagaagttt ttcacagggt atcctctaat 950  
tgataattat tcctatagag gattttacca aaaaacccat atttcttacc 1000  
aggagtatcc tttcaagggt tccctccat actgcagtgg gttgggttat 1050  
ataatgtcca gagatttggg gccaaagatc tatgaaatga tgggtcacgt 1100  
aaaaccctac aagtttgaag atgtttatgt cgggatctgt ttgaatttat 1150  
taaaagtga cattcatatt ccagaagaca caaatctttt ctttctatat 1200  
agaatccatt tggatgtctg tcaactgaga cgtgtgattg cagcccatgg 1250  
cttttcttcc aaggagatca tcactttttg gcaggtcatg ctaagggaaca 1300  
ccacatgcca ttattaactt cacattctac aaaaagccta gaaggacagg 1350  
ataccttgtg gaaagtgtta aataaagtag gtactgtgga aaattcatgg 1400  
ggaggtcagt gtgctggctt aactgaact gaaactcatg aaaaaccag 1450  
actggagact ggagggttac acttgtgatt tattagttag gcccttcaaa 1500

gatgatattgt ggaggaatta aatataaagg aattggaggt ttttgcataa 1550  
 gaaattaata ggaccaaaaca atttggacat gtcattctgt agactagaat 1600  
 ttcttaaaag ggtgttactg agttataagc tcactaggct gtaaaaacaa 1650  
 aacaatgtag agttttattt attgaacaat gtagtcactt gaagggtttg 1700  
 tgtatatctt atgtggatta ccaatttaaa aatatatgta gttctgtgtc 1750  
 aaaaaacttc ttactgaag ttatactgaa caaaatttta cctgtttttg 1800  
 gtcatttata aagtacttca agatgttgca gtatttcaca gttattatta 1850  
 tttaaaatta ctccaacttt gtgtttttaa atgttttgac gatttcaata 1900  
 caagataaaa aggatagtga atcattcttt acatgcaaac attttccagt 1950  
 tacttaactg atcagtttat tattgataca tcactccatt aatgtaaagt 2000  
 cataggtcat tattgcatat cagtaatctc ttggactttg ttaaatattt 2050  
 tactgtggtg atatagagaa gaattaaagc aagaaaatct gaaaa 2095

<210> 209  
 <211> 331  
 <212> PRT  
 <213> Homo sapiens

<400> 209  
 Met Ala Ser Ala Leu Trp Thr Val Leu Pro Ser Arg Met Ser Leu  
 1 5 10 15  
 Arg Ser Leu Lys Trp Ser Leu Leu Leu Leu Ser Leu Leu Ser Phe  
 20 25 30  
 Phe Val Met Trp Tyr Leu Ser Leu Pro His Tyr Asn Val Ile Glu  
 35 40 45  
 Arg Val Asn Trp Met Tyr Phe Tyr Glu Tyr Glu Pro Ile Tyr Arg  
 50 55 60  
 Gln Asp Phe His Phe Thr Leu Arg Glu His Ser Asn Cys Ser His  
 65 70 75  
 Gln Asn Pro Phe Leu Val Ile Leu Val Thr Ser His Pro Ser Asp  
 80 85 90  
 Val Lys Ala Arg Gln Ala Ile Arg Val Thr Trp Gly Glu Lys Lys  
 95 100 105  
 Ser Trp Trp Gly Tyr Glu Val Leu Thr Phe Phe Leu Leu Gly Gln  
 110 115 120  
 Glu Ala Glu Lys Glu Asp Lys Met Leu Ala Leu Ser Leu Glu Asp  
 125 130 135  
 Glu His Leu Leu Tyr Gly Asp Ile Ile Arg Gln Asp Phe Leu Asp  
 140 145 150  
 Thr Tyr Asn Asn Leu Thr Leu Lys Thr Ile Met Ala Phe Arg Trp  
 155 160 165

Val Thr Glu Phe	Cys Pro Asn Ala Lys Tyr	Val Met Lys Thr Asp
170	175	180
Thr Asp Val Phe	Ile Asn Thr Gly Asn Leu Val Lys Tyr Leu Leu	
185	190	195
Asn Leu Asn His	Ser Glu Lys Phe Phe Thr Gly Tyr Pro Leu Ile	
200	205	210
Asp Asn Tyr Ser	Tyr Arg Gly Phe Tyr Gln Lys Thr His Ile Ser	
215	220	225
Tyr Gln Glu Tyr	Pro Phe Lys Val Phe Pro Pro Tyr Cys Ser Gly	
230	235	240
Leu Gly Tyr Ile	Met Ser Arg Asp Leu Val Pro Arg Ile Tyr Glu	
245	250	255
Met Met Gly His	Val Lys Pro Ile Lys Phe Glu Asp Val Tyr Val	
260	265	270
Gly Ile Cys Leu	Asn Leu Leu Lys Val Asn Ile His Ile Pro Glu	
275	280	285
Asp Thr Asn Leu	Phe Phe Leu Tyr Arg Ile His Leu Asp Val Cys	
290	295	300
Gln Leu Arg Arg	Val Ile Ala Ala His Gly Phe Ser Ser Lys Glu	
305	310	315
Ile Ile Thr Phe	Trp Gln Val Met Leu Arg Asn Thr Thr Cys His	
320	325	330
Tyr		

<210> 210  
 <211> 745  
 <212> DNA  
 <213> Homo sapiens

<400> 210  
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 gtgtgacttc ttggagtctt tctagctcct gccctagcta actataatat 100  
 caacgtcaat gatgacaaca acaatgctgg aagtgggacag cagtcaagtga 150  
 gtgtcaacaa tgaacacaat gtggccaatg ttgacaataa caacggatgg 200  
 gactcctgga attccatctg ggattatgga aatggctttg ctgcaaccag 250  
 actctttcaa aagaagacat gcattgtgca caaatgaac aaggaaagtc 300  
 tgcctcccat tcaatccctt gatgcaactgg tcaaggaaaa gaagcttcag 350  
 ggtaaggggac caggaggacc acctccaag ggcctgatgt actcagtcaa 400  
 cccaaacaaa gtcgatgacc tgagcaagtt cggaaaaaac attgcaaaaa 450  
 tgtgtcgtgg gattccaaca tacatggctg aggagatgca agagggaagc 500  
 ctgttttttt actcaggaac gtgctacacg accagtgtac tatggattgt 550

ggacatttcc ttctgtggag acacggtgga gaactaaaca attttttaaa 600  
gccactatg atttagtcat ctgaatatgc tgtgcagaaa aaatattggc 650  
tccagtggtt ttaccatgt cattctgaaa tttttoteta ctagttagt 700  
ttgatttctt taagtttcaa taaaatcatt tagcattgaa aaaaa 745

<210> 211  
<211> 185  
<212> PRT  
<213> Homo sapiens

<400> 211  
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Ala Pro Ala Leu Ala Asn Tyr Asn Ile Asn Val Asn Asp Asp Asn  
20 25 30  
Asn Asn Ala Gly Ser Gly Gln Gln Ser Val Ser Val Asn Asn Glu  
35 40 45  
His Asn Val Ala Asn Val Asp Asn Asn Asn Gly Trp Asp Ser Trp  
50 55 60  
Asn Ser Ile Trp Asp Tyr Gly Asn Gly Phe Ala Ala Thr Arg Leu  
65 70 75  
Phe Gln Lys Lys Thr Cys Ile Val His Lys Met Asn Lys Glu Val  
80 85 90  
Met Pro Ser Ile Gln Ser Leu Asp Ala Leu Val Lys Glu Lys Lys  
95 100 105  
Leu Gln Gly Lys Gly Pro Gly Gly Pro Pro Pro Lys Gly Leu Met  
110 115 120  
Tyr Ser Val Asn Pro Asn Lys Val Asp Asp Leu Ser Lys Phe Gly  
125 130 135  
Lys Asn Ile Ala Asn Met Cys Arg Gly Ile Pro Thr Tyr Met Ala  
140 145 150  
Glu Glu Met Gln Glu Ala Ser Leu Phe Phe Tyr Ser Gly Thr Cys  
155 160 165  
Tyr Thr Thr Ser Val Leu Trp Ile Val Asp Ile Ser Phe Cys Gly  
170 175 180  
Asp Thr Val Glu Asn  
185

<210> 212  
<211> 1706  
<212> DNA  
<213> Homo sapiens

<400> 212  
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atgaaataat ttaaaagggc ttcgctcata tataggaaaa tcgcatatgg 150  
 tcctagtatt aaattcttat tgcttactga tttttttgag ttaagagttg 200  
 ttatatgcta gaatatgagg atgtgaatat aaataagaga agaaaaaaga 250  
 ataaagtaga ttgagtcctc aatttttatgt aagcttcaga agaaactggt 300  
 tgtttacatg caagcttata gttgaaatat ttttcaggaa ttacatgaat 350  
 gacagtcctc gaaccaatgt gttgttcga tttcaaccag agactatagc 400  
 atgtgcttgc atctacctg cagctagagc acttcagatt cgttgccaa 450  
 ctctgcccc ttggtttctt ctttttggtta ctacagaaga ggaaatccag 500  
 gaaatctgca tagaaacact taggctttat accgaaaaaa agccaaaacta 550  
 tgaattactg gaaaaagaag tagaaaaaag aaaagtagcc ttacaagaag 600  
 ccaaattaaa agcaaaggga ttgaatccgg atggaactcc agccctttca 650  
 accctgggtg gattttctcc agcctccaag ccatcatcac caagagaagt 700  
 aaaagctgaa gagaaatcac caatctccat taatgtgaag acagtcaaaa 750  
 aagaacctga ggatagacaa caggcttcca aaagccctta caatgggtga 800  
 agaaaagaca gcaagagaag tagaaatagc agaagtgcaa gtcgatcgag 850  
 gtcaagaaca cgatcacgtt ctatgcaca tactccaaga agacactata 900  
 ataataggcg gagtgcgtct ggaacataca gtcgagatc aagaagcagg 950  
 tcccgagctc acagtgaaag cctcgaaga catcataatc atggttctcc 1000  
 tcaccttaag gccaaagcata ccagagatga tttaaaaagt tcaaacagac 1050  
 atggtcataa aaggaaaaaa tctcgttctc gatctcagag caagtctcgg 1100  
 gatcactcag atgcagccaa gaaacacagg catgaaaggg gacatcatag 1150  
 ggacaggcgt gaacgatctc gctcctttga gaggtcccat aaaagcaagc 1200  
 accatgggtg cagtcgctca ggacatggca ggcacaggcg ctgactttct 1250  
 ctctccttga gctgcacaa gttcttggtt ttgcctatct acagtgatgat 1300  
 gtatggactc aatcaaaaa attaaaacga aactgattag gatttgattt 1350  
 cttgaaaccc tctaggtctc tagaactctg aggacagttt cttttgaaaa 1400  
 gaactatggt aatttttttg cacattaaaa tgccctagca gtatctaatt 1450  
 aaaaaccatg gtcaggttca attgtacttt attatagttg tgtattgttt 1500  
 attgctataa gaactggagc gtgaattctg taaaaatgta tottattttt 1550  
 atacagataa aattgcagac actgttctat ttaagtgggt atttgtttaa 1600  
 atgatgggtg atactttctt aacactgggt tgcctgcatg tgtaaaagatt 1650  
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aaaagt 1706

<210> 213

<211> 299

<212> PRT

<213> Homo sapiens

<400> 213

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Glu Thr Ile Ala Cys Ala Cys Ile Tyr Leu Ala Ala Arg Ala Leu  
20 25 30  
Gln Ile Pro Leu Pro Thr Arg Pro His Trp Phe Leu Leu Phe Gly  
35 40 45  
Thr Thr Glu Glu Glu Ile Gln Glu Ile Cys Ile Glu Thr Leu Arg  
50 55 60  
Leu Tyr Thr Arg Lys Lys Pro Asn Tyr Glu Leu Leu Glu Lys Glu  
65 70 75  
Val Glu Lys Arg Lys Val Ala Leu Gln Glu Ala Lys Leu Lys Ala  
80 85 90  
Lys Gly Leu Asn Pro Asp Gly Thr Pro Ala Leu Ser Thr Leu Gly  
95 100 105  
Gly Phe Ser Pro Ala Ser Lys Pro Ser Ser Pro Arg Glu Val Lys  
110 115 120  
Ala Glu Glu Lys Ser Pro Ile Ser Ile Asn Val Lys Thr Val Lys  
125 130 135  
Lys Glu Pro Glu Asp Arg Gln Gln Ala Ser Lys Ser Pro Tyr Asn  
140 145 150  
Gly Val Arg Lys Asp Ser Lys Arg Ser Arg Asn Ser Arg Ser Ala  
155 160 165  
Ser Arg Ser Arg Ser Arg Thr Arg Ser Arg Ser Arg Ser His Thr  
170 175 180  
Pro Arg Arg His Tyr Asn Asn Arg Arg Ser Arg Ser Gly Thr Tyr  
185 190 195  
Ser Ser Arg Ser Arg Ser Arg Ser Arg Ser His Ser Glu Ser Pro  
200 205 210  
Arg Arg His His Asn His Gly Ser Pro His Leu Lys Ala Lys His  
215 220 225  
Thr Arg Asp Asp Leu Lys Ser Ser Asn Arg His Gly His Lys Arg  
230 235 240  
Lys Lys Ser Arg Ser Arg Ser Gln Ser Lys Ser Arg Asp His Ser  
245 250 255  
Asp Ala Ala Lys Lys His Arg His Glu Arg Gly His His Arg Asp  
260 265 270  
Arg Arg Glu Arg Ser Arg Ser Phe Glu Arg Ser His Lys Ser Lys



His His Gly Gly Ser Arg Ser Gly His Gly Arg His Arg Arg  
290 295

<210> 214

<211> 730

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 72-73, 85, 91, 127, 226, 268, 454, 484, 513, 566, 663

<223> unknown base

<400> 214

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gcattgcttt ttacagaaat atattanctt tttagagtaa tttctagttt 150  
ggattgtaat atgaaattat ttaaaagggc ttgcctcata tataggaaaa 200  
tcgcatatgg tcctagtatt aaattnttat tgcttactga ttttttgag 250  
ttaagagttg ttatatgnta gaatatgagg atgtgaatat aaataagaga 300  
agaaaaaaga ataaagtaga ttgagctcc aattttatgt aagcttcaga 350  
agaactgggt tgtttacatg caagcttata gttgaaatat ttttcaggaa 400  
ttacatgaat gacagctctc gaaccaatgt gttgttcga tttcaaccag 450  
agantatagc atgtgcttgc atctacctg cagntagagc acttcagatt 500  
ccgttgccaa ctngtcccca ttggttctt ctttttggtg ctacagaaga 550  
ggaaatccag gaaatntgca tagaaacact taggctttat accagaaaaa 600  
agccaaaacta tgaattactg gaaaaagaag tagaaaaag aaaagtagcc 650  
ttacaagaag ccnaattaaa agcaaaggga ttgaatccgg atggaactcc 700  
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<210> 215

<211> 1807

<212> DNA

<213> Homo sapiens

<400> 215

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ccaccctcat gcacaggctg gcgccacact gctccttgcg gcgctggctg 150  
ctctgtaacg gcagtttgtt ccgatacaag caccgctcg aggaggagct 200  
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ccaatggcct tagtgaggag aagccactgt ctgtgcccc agatgccccg 300

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gcgtgtacct cttcacagag gcctactact acatgctggg accagccaag 450  
gagactaaca ttgctgtgtt ctgggtgcctg ctcacgggtga ccttctccat 500  
caagatgttc ctgacagtga cacggctgta cttcagcgcc gaggaggggg 550  
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atgagggttc cgaggccatt gtctccgaag cgtatgtgcc aggtttgagt 1750  
ggcgagggtg atgctggctg ctcttctgaa caaataaagg agcatgccga 1800  
tttttaa 1807

<210> 216

<211> 479  
 <212> PRT  
 <213> Homo sapiens

<400> 216

Met	Ala	Val	Leu	Gly	Val	Gln	Leu	Val	Val	Thr	Leu	Leu	Thr	Ala	1	5	10	15
Thr	Leu	Met	His	Arg	Leu	Ala	Pro	His	Cys	Ser	Phe	Ala	Arg	Trp	20	25	30	
Leu	Leu	Cys	Asn	Gly	Ser	Leu	Phe	Arg	Tyr	Lys	His	Pro	Ser	Glu	35	40	45	
Glu	Glu	Leu	Arg	Ala	Leu	Ala	Gly	Lys	Pro	Arg	Pro	Arg	Gly	Arg	50	55	60	
Lys	Glu	Arg	Trp	Ala	Asn	Gly	Leu	Ser	Glu	Glu	Lys	Pro	Leu	Ser	65	70	75	
Val	Pro	Arg	Asp	Ala	Pro	Phe	Gln	Leu	Glu	Thr	Cys	Pro	Leu	Thr	80	85	90	
Thr	Val	Asp	Ala	Leu	Val	Leu	Arg	Phe	Phe	Leu	Glu	Tyr	Gln	Trp	95	100	105	
Phe	Val	Asp	Phe	Ala	Val	Tyr	Ser	Gly	Gly	Val	Tyr	Leu	Phe	Thr	110	115	120	
Glu	Ala	Tyr	Tyr	Tyr	Met	Leu	Gly	Pro	Ala	Lys	Glu	Thr	Asn	Ile	125	130	135	
Ala	Val	Phe	Trp	Cys	Leu	Leu	Thr	Val	Thr	Phe	Ser	Ile	Lys	Met	140	145	150	
Phe	Leu	Thr	Val	Thr	Arg	Leu	Tyr	Phe	Ser	Ala	Glu	Glu	Gly	Gly	155	160	165	
Glu	Arg	Ser	Val	Cys	Leu	Thr	Phe	Ala	Phe	Leu	Phe	Leu	Leu	Leu	170	175	180	
Ala	Met	Leu	Val	Gln	Val	Val	Arg	Glu	Glu	Thr	Leu	Glu	Leu	Gly	185	190	195	
Leu	Glu	Pro	Gly	Leu	Ala	Ser	Met	Thr	Gln	Asn	Leu	Glu	Pro	Leu	200	205	210	
Leu	Lys	Lys	Gln	Gly	Trp	Asp	Trp	Ala	Leu	Pro	Val	Ala	Lys	Leu	215	220	225	
Ala	Ile	Arg	Val	Gly	Leu	Ala	Val	Val	Gly	Ser	Val	Leu	Gly	Ala	230	235	240	
Phe	Leu	Thr	Phe	Pro	Gly	Leu	Arg	Leu	Ala	Gln	Thr	His	Arg	Asp	245	250	255	
Ala	Leu	Thr	Met	Ser	Glu	Asp	Arg	Pro	Met	Leu	Gln	Phe	Leu	Leu	260	265	270	
His	Thr	Ser	Phe	Leu	Ser	Pro	Leu	Phe	Ile	Leu	Trp	Leu	Trp	Thr	275	280	285	
Lys	Pro	Ile	Ala	Arg	Asp	Phe	Leu	His	Gln	Pro	Pro	Phe	Gly	Glu				

	290	295	300
Thr Arg Phe Ser	Leu Leu Ser Asp Ser	Ala Phe Asp Ser Gly Arg	
	305	310	315
Leu Trp Leu Leu	Val Val Leu Cys Leu	Leu Arg Leu Ala Val Thr	
	320	325	330
Arg Pro His Leu	Gln Ala Tyr Leu Cys	Leu Ala Lys Ala Arg Val	
	335	340	345
Glu Gln Leu Arg	Arg Glu Ala Gly Arg	Ile Glu Ala Arg Glu Ile	
	350	355	360
Gln Gln Arg Val	Val Arg Val Tyr Cys	Tyr Val Thr Val Val Ser	
	365	370	375
Leu Gln Tyr Leu	Thr Pro Leu Ile Leu	Thr Leu Asn Cys Thr Leu	
	380	385	390
Leu Leu Lys Thr	Leu Gly Gly Tyr Ser	Trp Gly Leu Gly Pro Ala	
	395	400	405
Pro Leu Leu Ser	Pro Asp Pro Ser Ser	Ala Ser Ala Ala Pro Ile	
	410	415	420
Gly Ser Gly Glu	Asp Glu Val Gln Gln	Thr Ala Ala Arg Ile Ala	
	425	430	435
Gly Ala Leu Gly	Gly Leu Leu Thr Pro	Leu Phe Leu Arg Gly Val	
	440	445	450
Leu Ala Tyr Leu	Ile Trp Trp Thr Ala	Ala Cys Gln Leu Leu Ala	
	455	460	465
Ser Leu Phe Gly	Leu Tyr Phe His Gln	His Leu Ala Gly Ser	
	470	475	

<210> 217  
 <211> 574  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 5, 146  
 <223> unknown base

<400> 217  
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 ggaggagctt cgggccctgg cggggaagcc gaggcccgaga ggcaggaaaag 200  
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actcgggcgg cgtgtacctc ttcacagagg cctactacta catgctggga 400  
 ccagccaagg agactaacat tgctgtgttc tggtgccctg tcacagtgac 450  
 cttctccatc aagatgttcc tgacagtgac acggctgtac ttcagcgccg 500  
 agggaggggg tgagcgctct gtctgcctca cctttgcctt cctcttctg 550  
 ctgctggcca tgctgtgtca agcg 574

<210> 218  
 <211> 2571  
 <212> DNA  
 <213> Homo sapiens

<400> 218  
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 ttgtgatcta ctgattgtgg gggcatggca aggtttgctt aaaggagctt 150  
 ggctggtttg ggcctctgta gctgacagaa ggtggccagg gagaatgcag 200  
 cacactgctc ggagaatgaa ggcgcttctg ttgctggtct tgccttggct 250  
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 cagaactctg taaagtgccc tccactacg gcctgaccaa agatagggaag 350  
 aggcgctcac aagatggctg tccagacggc tgtgcgagcc toacagccac 400  
 ggctccctcc ccagagggtt ctgcagctgc caccatctcc ttaatgacag 450  
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 cagccagcaa tcagcccagt ggactctggc cggagcaacc gaactagggc 550  
 acggcccttt gagagatcca ctattagaag cagatcattt aaaaaataa 600  
 atcgagcttt gagtgttctt cgaaggacaa agagcgggag tgcagttgcc 650  
 aacctgccc accagggcag ggaaaattct gaaaacacca ctgccctga 700  
 agtctttcca aggttgtagc acctgattcc agatggtgaa attaccagca 750  
 tcaagatcaa tcgagtagat ccagtgaaa gcctctctat taggctggtg 800  
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 taaaggatcaa cgggatggac atcagcaatg tccctcacia ctacgctgtg 950  
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 ccagaaagtg cggtcatct gattcaggcc agtgaagac gtgttcacct 1300  
 cgctgtgtcc cgccaggttc ggccaggag ccctgacatc ttccaggag 1350  
 ccggtctgaa cagcaatggc agctgggtccc cagggccagg ggagaggagc 1400  
 aacactccca agcccccca tcctacaatt acttgtcatg agaaggtggt 1450  
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 gagcatcaca tagagaatgg gatttgccca tctatgtcat cagtgttgag 1550  
 cccggaggag tcataagcag agatggaaga ataaaaacag gtgacatttt 1600  
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 caccagcata caatgatgga agaattagat gtgggtgat tcttctgtct 2000  
 gtcaatggta gaagtacatc aggaatgata catgctgtct tggcaagact 2050  
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 gcacttttt atagaatcaa tgatgggtca gaggaaaaca gaaaaatcac 2150  
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 ttaaagaaag aatacattgt aaaaatgtca ggaaaagtat gatcatctaa 2250  
 tgaaagccag ttacacctca gaaaatatga ttccaaaaaa attaaaacta 2300  
 ctagttttt ttcatgttg aggatttctc attactctac aacattgttt 2350  
 atattttttc tattcaataa aaagccctaa aacaactaaa atgattgatt 2400  
 tgtatacccc actgaattca agctgattta aatttaaaat ttggtatatg 2450  
 ctgaagtctg ccaagggtac attatggcca tttttaattt acagctaaaa 2500  
 ttttttttaa aatgcattgc tgagaaacgt tgctttcatc aaacaagaat 2550  
 aaatattttt cagaagttaa a 2571

<210> 219

<211> 632

<212> PRT

<213> Homo sapiens

<400> 219

Met Lys Ala Leu Leu Leu Val Leu Pro Trp Leu Ser Pro Ala

1	5	10	15
Asn Tyr Ile Asp	Asn Val Gly Asn Leu	His Phe Leu Tyr Ser	Glu 30
	20	25	
Leu Cys Lys Gly	Ala Ser His Tyr Gly	Leu Thr Lys Asp Arg	Lys 45
	35	40	
Arg Arg Ser Gln	Asp Gly Cys Pro Asp	Gly Cys Ala Ser Leu Thr	60
	50	55	
Ala Thr Ala Pro	Ser Pro Glu Val Ser	Ala Ala Thr Ile Ser	75
	65	70	
Leu Met Thr Asp	Glu Pro Gly Leu Asp	Asn Pro Ala Tyr Val Ser	90
	80	85	
Ser Ala Glu Asp	Gly Gln Pro Ala Ile	Ser Pro Val Asp Ser	Gly 105
	95	100	
Arg Ser Asn Arg	Thr Arg Ala Arg Pro	Phe Glu Arg Ser Thr Ile	120
	110	115	
Arg Ser Arg Ser	Phe Lys Lys Ile Asn	Arg Ala Leu Ser Val Leu	135
	125	130	
Arg Arg Thr Lys	Ser Gly Ser Ala Val	Ala Asn His Ala Asp Gln	150
	140	145	
Gly Arg Glu Asn	Ser Glu Asn Thr Thr	Ala Pro Glu Val Phe Pro	165
	155	160	
Arg Leu Tyr His	Leu Ile Pro Asp Gly	Glu Ile Thr Ser Ile Lys	180
	170	175	
Ile Asn Arg Val	Asp Pro Ser Glu Ser	Leu Ser Ile Arg Leu Val	195
	185	190	
Gly Gly Ser Glu	Thr Pro Leu Val His	Ile Ile Ile Gln His Ile	210
	200	205	
Tyr Arg Asp Gly	Val Ile Ala Arg Asp	Gly Arg Leu Leu Pro Gly	225
	215	220	
Asp Ile Ile Leu	Lys Val Asn Gly Met	Asp Ile Ser Asn Val Pro	240
	230	235	
His Asn Tyr Ala	Val Arg Leu Leu Arg	Gln Pro Cys Gln Val Leu	255
	245	250	
Trp Leu Thr Val	Met Arg Glu Gln Lys	Phe Arg Ser Arg Asn Asn	270
	260	265	
Gly Gln Ala Pro	Asp Ala Tyr Arg Pro	Arg Asp Asp Ser Phe His	285
	275	280	
Val Ile Leu Asn	Lys Ser Ser Pro Glu	Glu Gln Leu Gly Ile Lys	300
	290	295	
Leu Val Arg Lys	Val Asp Glu Pro Gly	Val Phe Ile Phe Asn Val	315
	305	310	
Leu Asp Gly Gly	Val Ala Tyr Arg His	Gly Gln Leu Glu Glu Asn	

	320		325		330
Asp Arg Val Leu	Ala Ile Asn Gly His	Asp Leu Arg Tyr Gly	Ser		
	335		340		345
Pro Glu Ser Ala	Ala His Leu Ile Gln	Ala Ser Glu Arg Arg	Val		
	350		355		360
His Leu Val Val	Ser Arg Gln Val Arg	Gln Arg Ser Pro Asp	Ile		
	365		370		375
Phe Gln Glu Ala	Gly Trp Asn Ser Asn	Gly Ser Trp Ser Pro	Gly		
	380		385		390
Pro Gly Glu Arg	Ser Asn Thr Pro Lys	Pro Leu His Pro Thr	Ile		
	395		400		405
Thr Cys His Glu	Lys Val Val Asn Ile	Gln Lys Asp Pro Gly	Glu		
	410		415		420
Ser Leu Gly Met	Thr Val Ala Gly Gly	Ala Ser His Arg Glu	Trp		
	425		430		435
Asp Leu Pro Ile	Tyr Val Ile Ser Val	Glu Pro Gly Gly Val	Ile		
	440		445		450
Ser Arg Asp Gly	Arg Ile Lys Thr Gly	Asp Ile Leu Leu Asn	Val		
	455		460		465
Asp Gly Val Glu	Leu Thr Glu Val Ser	Arg Ser Glu Ala Val	Ala		
	470		475		480
Leu Leu Lys Arg	Thr Ser Ser Ser Ile	Val Leu Lys Ala Leu	Glu		
	485		490		495
Val Lys Glu Tyr	Glu Pro Gln Glu Asp	Cys Ser Ser Pro Ala	Ala		
	500		505		510
Leu Asp Ser Asn	His Asn Met Ala Pro	Pro Ser Asp Trp Ser	Pro		
	515		520		525
Ser Trp Val Met	Trp Leu Glu Leu Pro	Arg Cys Leu Tyr Asn	Cys		
	530		535		540
Lys Asp Ile Val	Leu Arg Arg Asn Thr	Ala Gly Ser Leu Gly	Phe		
	545		550		555
Cys Ile Val Gly	Gly Tyr Glu Glu Tyr	Asn Gly Asn Lys Pro	Phe		
	560		565		570
Phe Ile Lys Ser	Ile Val Glu Gly Thr	Pro Ala Tyr Asn Asp	Gly		
	575		580		585
Arg Ile Arg Cys	Gly Asp Ile Leu Leu	Ala Val Asn Gly Arg	Ser		
	590		595		600
Thr Ser Gly Met	Ile His Ala Cys Leu	Ala Arg Leu Leu Lys	Glu		
	605		610		615
Leu Lys Gly Arg	Ile Thr Leu Thr Ile	Val Ser Trp Pro Gly	Thr		
	620		625		630
Phe Leu					



<210> 220  
 <211> 773  
 <212> DNA  
 <213> Homo sapiens

<400> 220  
 ccaaagtgat catttgaaaa agagatatcc acatcttcaa gcccatataa 50  
 aggatagaag ctgcacaggg cagctttact tactccagca ccttcctctc 100  
 ccaggcaaat ggtgctgacc atctttggga tacaatctca tggatacgag 150  
 gttttaaca tcatacagcc aagcaacaat ggtggcaatg ttcaggagac 200  
 agtgacaatt gataatgaaa aaaataccgc catcggttaac atccatgcag 250  
 gatcatgctc ttctaccaca atttttgact ataaacatgg ctacattgca 300  
 tccagggtgc tctccgaag agcctgcttt atcctgaaga tggaccatca 350  
 gaacatccct cctctgaaca atctccaatg gtacatctat gagaaacagg 400  
 ctctggacaa catgttctcc aacaaatata cctgggtcaa gtacaaccct 450  
 ctggagcttc tgatcaaaga cgtggattgg ttctgcttg ggtcacccat 500  
 tgagaaactc tgcaaacata tcctttgta taagggggaa gtggttgaaa 550  
 acacacataa tgcoggtgct ggaggctgtg caaaggctgg gctcctgggc 600  
 atcttgggaa tttcaatctg tgcagacatt catgtttagg atgattagcc 650  
 ctctgttttt atcttttcaa agaaatacat ccttggttta cactcaaaag 700  
 tcaaattaaa ttctttccca atgccccaac taattttgag attcagtcag 750  
 aaaatataaa tgctgtatatt ata 773

<210> 221  
 <211> 184  
 <212> PRT  
 <213> Homo sapiens

<400> 221  
 Met Lys Ile Leu Val Ala Phe Leu Val Val Leu Thr Ile Phe Gly  
 1 5 10 15  
 Ile Gln Ser His Gly Tyr Glu Val Phe Asn Ile Ile Ser Pro Ser  
 20 25 30  
 Asn Asn Gly Gly Asn Val Gln Glu Thr Val Thr Ile Asp Asn Glu  
 35 40 45  
 Lys Asn Thr Ala Ile Val Asn Ile His Ala Gly Ser Cys Ser Ser  
 50 55 60  
 Thr Thr Ile Phe Asp Tyr Lys His Gly Tyr Ile Ala Ser Arg Val  
 65 70 75  
 Leu Ser Arg Arg Ala Cys Phe Ile Leu Lys Met Asp His Gln Asn  
 80 85 90

Ile Pro Pro Leu Asn Asn Leu Gln Trp Tyr Ile Tyr Glu Lys Gln  
95 100 105

Ala Leu Asp Asn Met Phe Ser Asn Lys Tyr Thr Trp Val Lys Tyr  
110 115 120

Asn Pro Leu Glu Ser Leu Ile Lys Asp Val Asp Trp Phe Leu Leu  
125 130 135

Gly Ser Pro Ile Glu Lys Leu Cys Lys His Ile Pro Leu Tyr Lys  
140 145 150

Gly Glu Val Val Glu Asn Thr His Asn Val Gly Ala Gly Gly Cys  
155 160 165

Ala Lys Ala Gly Leu Leu Gly Ile Leu Gly Ile Ser Ile Cys Ala  
170 175 180

Asp Ile His Val

<210> 222

<211> 992

<212> DNA

<213> Homo sapiens

<400> 222

ggcacgagcc aggaactagg aggtttctcac tgcccagaca gaggccctac 50

accacaccag gcattggggct ccctgggctg ttctgcttgg ccgtgctggc 100

tgccagagc ttctccaagg cacgggagga agaaattacc cctgtgtctc 150

ccattgccta caaagtctct gaagttttcc ccaaaggccg ctgggtgctc 200

ataacctgct gtgcaccca gccaccaccg cccatcacct attccctctg 250

tggaaccaag aacatcaagg tggccaagaa ggtggtgaag acccagagc 300

cggcctcctt caacctcaac gtcacactca agtccagtc agacctgctc 350

acctacttct gccgggcgtc ctccacctca ggtgcccatg tggacagtgc 400

caggctacag atgcactggg agctgtggtc caagccagtg tctgagctgc 450

gggccaact cactctgcag gacagagggg caggcccccag ggtggagatg 500

atttgccagg cgtcctcggg cagcccaact atcaccaaca gcctgatcgg 550

gaaggatggg cagggtccacc tgcagcagag accatgccac aggcagcctg 600

ccaacttctc ctctctgcg agccagacat cggactgggt ctggtgccag 650

gctgcaaaca acgccaatgt ccagcacagc gccttcacag tgggtccccc 700

aggtgtgtac cagaagatgg aggactggca gggccccctg gagagcccca 750

tccttgccct gccgctctac aggagcaccg gccgtctgag tgaagaggag 800

tttggggggg tcaggatagg gaatggggag gtcagaggac gcaaagcagc 850

agccatgtag aatgaacctg ccagagagcc aagcacggca gaggactgca 900

ggccatcagc gtgcactgtt cgtatttga gtccatgcaa aatgagtgtg 950

ttttagctgc tcttgccaca aaaaaaaaaa aaaaaaaaaa aa 992

<210> 223

<211> 265

<212> PRT

<213> Homo sapiens

<400> 223

Met Gly Leu Pro Gly Leu Phe Cys Leu Ala Val Leu Ala Ala Ser  
1 5 10 15

Ser Phe Ser Lys Ala Arg Glu Glu Ile Thr Pro Val Val Ser  
20 25 30

Ile Ala Tyr Lys Val Leu Glu Val Phe Pro Lys Gly Arg Trp Val  
35 40 45

Leu Ile Thr Cys Cys Ala Pro Gln Pro Pro Pro Ile Thr Tyr  
50 55 60

Ser Leu Cys Gly Thr Lys Asn Ile Lys Val Ala Lys Lys Val Val  
65 70 75

Lys Thr His Glu Pro Ala Ser Phe Asn Leu Asn Val Thr Leu Lys  
80 85 90

Ser Ser Pro Asp Leu Leu Thr Tyr Phe Cys Arg Ala Ser Ser Thr  
95 100 105

Ser Gly Ala His Val Asp Ser Ala Arg Leu Gln Met His Trp Glu  
110 115 120

Leu Trp Ser Lys Pro Val Ser Glu Leu Arg Ala Asn Phe Thr Leu  
125 130 135

Gln Asp Arg Gly Ala Gly Pro Arg Val Glu Met Ile Cys Gln Ala  
140 145 150

Ser Ser Gly Ser Pro Pro Ile Thr Asn Ser Leu Ile Gly Lys Asp  
155 160 165

Gly Gln Val His Leu Gln Gln Arg Pro Cys His Arg Gln Pro Ala  
170 175 180

Asn Phe Ser Phe Leu Pro Ser Gln Thr Ser Asp Trp Phe Trp Cys  
185 190 195

Gln Ala Ala Asn Asn Ala Asn Val Gln His Ser Ala Leu Thr Val  
200 205 210

Val Pro Pro Gly Gly Asp Gln Lys Met Glu Asp Trp Gln Gly Pro  
215 220 225

Leu Glu Ser Pro Ile Leu Ala Leu Pro Leu Tyr Arg Ser Thr Arg  
230 235 240

Arg Leu Ser Glu Glu Glu Phe Gly Gly Phe Arg Ile Gly Asn Gly  
245 250 255

Glu Val Arg Gly Arg Lys Ala Ala Ala Met  
260 265

<210> 224  
 <211> 1297  
 <212> DNA  
 <213> Homo sapiens

<400> 224  
 ggtccttaat ggcagcagcc gccgctacca agatccttct gtgcctcccg 50  
 ctctctgtcc tgtgtcccg ctgggtcccg gctgggcgag ccgacctca 100  
 ctctctttgc tatgacatca ccgtcatccc taagttcaga cctggaccac 150  
 ggtggtgtgc ggttcaaggc cagggtgatg aaaagacttt tcttactat 200  
 gactgtggca acaagacagt cacacctgtc agtccctgg ggaagaaact 250  
 aaatgtcaca acggcctgga aagcacagaa ccagtgactg agagaggttg 300  
 tggacatact tacagagcaa ctgcgtgaca ttcagctgga gaattacaca 350  
 cccaaggaac cctcaccct gcaggcaagg atgtcttgtg agcagaaagc 400  
 tgaaggacac agcagtggat ctggcagtt cagtttctgat gggcagatct 450  
 tctcctctct tgactcagag aagagaatgt ggacaacggt teatctgga 500  
 gccagaaaga tgaagaaaa gtgggagaat gacaagggtg tggccatgtc 550  
 cttcattac ttctcaatgg gagactgtat aggatggctt gaggacttct 600  
 tgatgggcat ggacagcacc ctggagccaa gtgcaggagc accactcgcc 650  
 atgtctcag gcacaacca actcagggcc acagccacca cctcatcct 700  
 ttgctgcctc ctcatcatcc tccctgctt catctcctt ggcatctgag 750  
 gagagtcctt tagagtgaca ggttaaagct gataccaaaa ggctcctgtg 800  
 agcaoggtct tgatcaaaact cgcccttctg tctggccagc tgcccacgac 850  
 ctacggtgta tgtccagtgg cctccagcag atcatgatga catcatggac 900  
 ccaatagctc attcactgcc ttgattcctt ttgocaaaca ttttaccagc 950  
 agttatacct aacatattat gcaattttct ctgtgtgcta cotgatggaa 1000  
 ttctgcact taaagttctg gctgactaaa caagatatat cattttcttt 1050  
 ctctctttt tgtttggaaa atcaagtact tctttgaatg atgatctctt 1100  
 tcttgcaaat gatattgtca gtaaaataat caggttagac ttcagacctc 1150  
 tggggattct ttccgtgtcc tgaagagaa tttttaaatt atttaataag 1200  
 aaaaaattta tattaatgat tgtttccttt agtaatttat tgtctgtac 1250  
 tgatatttaa ataaagagt ctatttccca aaaaaaaaa aaaaaaa 1297

<210> 225  
 <211> 246  
 <212> PRT  
 <213> Homo sapiens

<400> 225

Met Ala Ala Ala Ala Thr Lys Ile Leu Leu Cys Leu Pro Leu  
1 5 10 15  
Leu Leu Leu Leu Ser Gly Trp Ser Arg Ala Gly Arg Ala Asp Pro  
20 25 30  
His Ser Leu Cys Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg Pro  
35 40 45  
Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr  
50 55 60  
Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser  
65 70 75  
Pro Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala Gln  
80 85 90  
Asn Pro Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu  
95 100 105  
Arg Asp Ile Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr  
110 115 120  
Leu Gln Ala Arg Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser  
125 130 135  
Ser Gly Ser Trp Gln Phe Ser Phe Asp Gly Gln Ile Phe Leu Leu  
140 145 150  
Phe Asp Ser Glu Lys Arg Met Trp Thr Thr Val His Pro Gly Ala  
155 160 165  
Arg Lys Met Lys Glu Lys Trp Glu Asn Asp Lys Val Val Ala Met  
170 175 180  
Ser Phe His Tyr Phe Ser Met Gly Asp Cys Ile Gly Trp Leu Glu  
185 190 195  
Asp Phe Leu Met Gly Met Asp Ser Thr Leu Glu Pro Ser Ala Gly  
200 205 210  
Ala Pro Leu Ala Met Ser Ser Gly Thr Thr Gln Leu Arg Ala Thr  
215 220 225  
Ala Thr Thr Leu Ile Leu Cys Cys Leu Leu Ile Ile Leu Pro Cys  
230 235 240  
Phe Ile Leu Pro Gly Ile  
245

<210> 226

<211> 735

<212> DNA

<213> Homo sapiens

<400> 226

gggaaagcca ttgcgaaaac ccatctatatac aaactatata ttttcatttc 50  
tgctgctagc tgccttgagg ctcacaattt tcattctgtt ttctgacttt 100  
caagttatat accgtggaat ggagttgatc ccaaccataa catcgtggag 150

gggttttaatt ttggtggtag ccctcaccca attctggtgt ggctttcttt 200  
 gcagaggatt ccaccttcaa aatcatgaac tctggctgtt gatcaaaaga 250  
 gaatttggat tctactctaa aagtcaatat aggacttggc aaaagaagct 300  
 agcagaagac tcaacctggc ctcccataaa caggacagat tattcagggtg 350  
 atggcaaaaa tggattotac atcaacggag gctatgaaag ccatgaacag 400  
 attccaaaaa gaaaaactcaa attggggaggc caaccacag aacagcattt 450  
 ctggggccagg ctgtaatcag aattgtcgtc gtacatgctc aacagcattg 500  
 cttttttccc caaaattaac acattgtgga gaagtgtga tactctcccc 550  
 ttacctttcc tctctccatt caagcattca aagtatattt tcaatgaatt 600  
 aaaccttgca gcaagggacc ttagataggc ttattctgac tgtatgcttt 650  
 accaatgaga gaaaaaaatg catttctctgt atcctccttt tcaataaact 700  
 gtattcattt tgaaaaaaaa aaaaaaaaaa aaaaa 735

<210> 227  
 <211> 115  
 <212> PRT  
 <213> Homo sapiens

<400> 227  
 Met Glu Leu Ile Pro Thr Ile Thr Ser Trp Arg Val Leu Ile Leu  
 1 5 10 15  
 Val Val Ala Leu Thr Gln Phe Trp Cys Gly Phe Leu Cys Arg Gly  
 20 25 30  
 Phe His Leu Gln Asn His Glu Leu Trp Leu Ile Lys Arg Glu  
 35 40 45  
 Phe Gly Phe Tyr Ser Lys Ser Gln Tyr Arg Thr Trp Gln Lys Lys  
 50 55 60  
 Leu Ala Glu Asp Ser Thr Trp Pro Pro Ile Asn Arg Thr Asp Tyr  
 65 70 75  
 Ser Gly Asp Gly Lys Asn Gly Phe Tyr Ile Asn Gly Gly Tyr Glu  
 80 85 90  
 Ser His Glu Gln Ile Pro Lys Arg Lys Leu Lys Leu Gly Gly Glu  
 95 100 105  
 Pro Thr Glu Gln His Phe Trp Ala Arg Leu  
 110 115

<210> 228  
 <211> 2185  
 <212> DNA  
 <213> Homo sapiens

<400> 228  
 gttctccttt ccgagccaaa atcccaggcg atgggtgaatt atgaacgtgc 50  
 cacaccatga agctcttctg gcaggtaact gtgcaccacc acacctgga 100

tgccatcctg ctcccgttcg tctacctcac ggcgcaagtg tggattctgt 150  
 gtgcagccat cgctgtgcc gctcagccg ggccccagaa ctgccccctc 200  
 gtttgctcgt gcagtaacca gttcagcaag gtggtgtgca cgcgccgggg 250  
 cctctccgag gtcccgcagg gtattccctc gaacaccccg tacttcaacc 300  
 tcatggagaa caacatccag atgatccagg ccgacacctt ccgccacctc 350  
 caccacctgg aggtcctgca gttgggcagg aactccatcc ggcagattga 400  
 ggtggggggc ttcaacggcc tggccagcct caacacctg gagctgttcg 450  
 acaactggct gacagtcac cctagcgggg cctttgaata cctgtccaag 500  
 ctgcccggagc tctggcttcg caacaacccc atcgaaagca tcccccttta 550  
 cgccctcaac cgggtgcctt cctcatgcg cctggacttg ggggagctca 600  
 agaagctgga gtatatctct gagggagctt ttgaggggct gttcaacctc 650  
 aagtatctga acttgggcat gtgcaacatt aaagacatgc ccaatctcac 700  
 ccccctgtg gggctggagg agctggagat gtcagggaac cacttccctg 750  
 agatcaggcc tggctccttc catggcctga gctccctcaa gaagctctgg 800  
 gtcatgaact cacaggctcag cctgattgag cggaatgctt ttgacgggct 850  
 ggcttcactt gtggaactca acttggccca caataacctc tcttctttgc 900  
 cccatgacct ctttaccctg ctgaggtacc tgggtgagtt gcatctacac 950  
 cacaacctt ggaactgtga ttgtgacatt ctgtggctag cctggtggct 1000  
 tcgagagtat ataccacca attccaactg ctgtggccgc tgtcatgctc 1050  
 ccatgcacat gcgaggccgc tacctcgttg aggtggacca ggcctccttc 1100  
 cagtgtcttg ccccttctat catggacgca cctcgagacc tcaacatttc 1150  
 tgagggctcg atggcagaac ttaagtgtcg gactccccct atgtcctcgc 1200  
 tgaagtgggt gctgccaat gggacagtcg tcagccacgc ctcccggcac 1250  
 ccaaggatct ctgtcctcaa cgacggcacc ttgaactttt ccaactgtct 1300  
 gctttcagac actgggggtg acacatgcat ggtgaccaat gttgcaggca 1350  
 actccaacgc ctgggctcac ctcaatgtga gcacgggtga gcttaacacc 1400  
 tccaactaca gcttcttcac cacagtaaca gtggagacca cggagatctc 1450  
 gcctgaggac acaacgcgaa agtacaagcc tgttcctacc acgtccactg 1500  
 gttaccagcc ggcataatcc acctctacca cgggtgctcat tcagactacc 1550  
 cgtgtgccca agcaggtggc agtaccgccg acagacacca ctgacaagat 1600  
 gcagaccagc ctggtgaag tcatgaagac caccaagatc atcattggct 1650  
 gcttttgagg agtgactctg ctgactgcgc ccatgttgat tgtctctat 1700

aaacttcgta agcggcacca gcagcggagt acagtcacag ccgcccgac 1750  
 tgttgagata atccaggtgg acgaagacat cccagcagca acatcccgag 1800  
 cagcaacagc agctccgtcc ggtgtatcag gtgagggggc agtagtgctg 1850  
 cccacaatto atgaccatat taactacaac acctacaaac cagcacatgg 1900  
 ggcccaatgg acagaaaaa gcttggggaa ctctctgcac cccacagtca 1950  
 coactatctc tgaaccttat ataattcaga cccataccaa ggacaaggta 2000  
 caggaaactc aaatatgact cccctccccc aaaaaactta taaaatgcaa 2050  
 tagaatgcac acaaagacag caacttttgt acagagtggg gagagacttt 2100  
 ttcttgata tgcttatata ttaagtctat gggctgggta aaaaaaacag 2150  
 attatattaa aatttaaaga caaaaagtca aaaca 2185

<210> 229  
 <211> 653  
 <212> PRT  
 <213> Homo sapiens

<400> 229  
 Met Lys Leu Leu Trp Gln Val Thr Val His His His Thr Trp Asn  
 1 5 10  
 Ala Ile Leu Leu Pro Phe Val Tyr Leu Thr Ala Gln Val Trp Ile  
 20 25 30  
 Leu Cys Ala Ala Ile Ala Ala Ala Ser Ala Gly Pro Gln Asn  
 35 40 45  
 Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val Val  
 50 55 60  
 Cys Thr Arg Arg Gly Leu Ser Glu Val Pro Gln Gly Ile Pro Ser  
 65 70 75  
 Asn Thr Arg Tyr Leu Asn Leu Met Glu Asn Asn Ile Gln Met Ile  
 80 85 90  
 Gln Ala Asp Thr Phe Arg His Leu His His Leu Glu Val Leu Gln  
 95 100 105  
 Leu Gly Arg Asn Ser Ile Arg Gln Ile Glu Val Gly Ala Phe Asn  
 110 115 120  
 Gly Leu Ala Ser Leu Asn Thr Leu Glu Leu Phe Asp Asn Trp Lys  
 125 130 135  
 Thr Val Ile Pro Ser Gly Ala Phe Glu Tyr Leu Ser Lys Leu Arg  
 140 145 150  
 Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser Tyr  
 155 160 165  
 Ala Phe Asn Arg Val Pro Ser Leu Met Arg Leu Asp Leu Gly Glu  
 170 175 180  
 Leu Lys Lys Leu Glu Tyr Ile Ser Glu Gly Ala Phe Glu Gly Leu



0000722: 440000

185	190	195
Phe Asn Leu Lys Tyr Leu Asn Leu Gly Met Cys Asn Ile Lys Asp		
200	205	210
Met Pro Asn Leu Thr Pro Leu Val Gly Leu Glu Glu Leu Glu Met		
215	220	225
Ser Gly Asn His Phe Pro Glu Ile Arg Pro Gly Ser Phe His Gly		
230	235	240
Leu Ser Ser Leu Lys Lys Leu Trp Val Met Asn Ser Gln Val Ser		
245	250	255
Leu Ile Glu Arg Asn Ala Phe Asp Gly Leu Ala Ser Leu Val Glu		
260	265	270
Leu Asn Leu Ala His Asn Asn Leu Ser Ser Leu Pro His Asp Leu		
275	280	285
Phe Thr Pro Leu Arg Tyr Leu Val Glu Leu His Leu His His Asn		
290	295	300
Pro Trp Asn Cys Asp Cys Asp Ile Leu Trp Leu Ala Trp Trp Leu		
305	310	315
Arg Glu Tyr Ile Pro Thr Asn Ser Thr Cys Cys Gly Arg Cys His		
320	325	330
Ala Pro Met His Met Arg Gly Arg Tyr Leu Val Glu Val Asp Gln		
335	340	345
Ala Ser Phe Gln Cys Ser Ala Pro Phe Ile Met Asp Ala Pro Arg		
350	355	360
Asp Leu Asn Ile Ser Glu Gly Arg Met Ala Glu Leu Lys Cys Arg		
365	370	375
Thr Pro Pro Met Ser Ser Val Lys Trp Leu Leu Pro Asn Gly Thr		
380	385	390
Val Leu Ser His Ala Ser Arg His Pro Arg Ile Ser Val Leu Asn		
395	400	405
Asp Gly Thr Leu Asn Phe Ser His Val Leu Leu Ser Asp Thr Gly		
410	415	420
Val Tyr Thr Cys Met Val Thr Asn Val Ala Gly Asn Ser Asn Ala		
425	430	435
Ser Ala Tyr Leu Asn Val Ser Thr Ala Glu Leu Asn Thr Ser Asn		
440	445	450
Tyr Ser Phe Phe Thr Thr Val Thr Val Glu Thr Thr Glu Ile Ser		
455	460	465
Pro Glu Asp Thr Thr Arg Lys Tyr Lys Pro Val Pro Thr Thr Ser		
470	475	480
Thr Gly Tyr Gln Pro Ala Tyr Thr Thr Ser Thr Thr Val Leu Ile		
485	490	495
Gln Thr Thr Arg Val Pro Lys Gln Val Ala Val Pro Ala Thr Asp		

500	505	510
Thr Thr Asp Lys Met Gln Thr Ser Leu Asp Glu Val Met Lys Thr		
515	520	525
Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Val Thr Leu Leu Ala		
530	535	540
Ala Ala Met Leu Ile Val Phe Tyr Lys Leu Arg Lys Arg His Gln		
545	550	555
Gln Arg Ser Thr Val Thr Ala Ala Arg Thr Val Glu Ile Ile Gln		
560	565	570
Val Asp Glu Asp Ile Pro Ala Ala Thr Ser Ala Ala Ala Thr Ala		
575	580	585
Ala Pro Ser Gly Val Ser Gly Glu Gly Ala Val Val Leu Pro Thr		
590	595	600
Ile His Asp His Ile Asn Tyr Asn Thr Tyr Lys Pro Ala His Gly		
605	610	615
Ala His Trp Thr Glu Asn Ser Leu Gly Asn Ser Leu His Pro Thr		
620	625	630
Val Thr Thr Ile Ser Glu Pro Tyr Ile Ile Gln Thr His Thr Lys		
635	640	645
Asp Lys Val Gln Glu Thr Gln Ile		
650		

<210> 230  
 <211> 2846  
 <212> DNA  
 <213> Homo sapiens

<400> 230  
 cgctcgggca ccagccgcgg caaggatgga gctgggttgc tggacgcagt 50  
 tggggctcac tttcttcag ctcttctca tctcgtcctt gccaaagagag 100  
 tacacagtca ttaatgaagc ctgccctgga gcagagtgga atatcatgtg 150  
 tcgggagtgc tgtgaatatg atcagattga gtgcgtctgc cccggaaaga 200  
 gggaagtctg ggttataacc atcccttgct gcaggaatga ggagaatgag 250  
 tgtgactcct gctgatcca ccaggttgt accatctttg aaaactgcga 300  
 gagctgccga aatggctcat ggggggttac cttggatgac ttctatgtga 350  
 aggggttcta ctgtgcagag tgccgagcag gctggtacgg aggagactgc 400  
 atgcgatgtg gccaggttct gcgagcccca aagggtcaga ttttgttgga 450  
 aagctatccc ctaaatgctc actgtgaatg gaccattcat gctaaccctg 500  
 ggtttgtcat ccaactaaga tttgtcatgt tgagtctgga gtttgactac 550  
 atgtgccagt atgactatgt tgaggttcgt gatggagaca accgcgatgg 600  
 ccagatcatc aagcgtgtct gtggcaacga gcggccagct cctatccaga 650

gcataggatc ctactccac gtcctcttcc actccgatgg ctccaagaat 700  
 tttgacgggt tccatgccat ttatgaggag atcacagcat gctctcacc 750  
 cccttgttcc catgacggca cgtgcgtcct tgacaaggct ggaatctaca 800  
 agtggtcctg cttggcaggc tatactgggc agcgtctga aaatctcctt 850  
 gaagaaagaa actgctcaga ccctgggggc ccagtcaatg ggtaccagaa 900  
 aataacaggg ggccctgggc ttatcaacgg acgccatgct aaaattggca 950  
 ccgtgtgtgc tttctttgt aacaactcct atgttcttag tggcaatgag 1000  
 aaaaagaact gccagcagaa tggagagtgg tcagggaac agcccatctg 1050  
 cataaaagcc tgccgagaac caaagatttc agacctggtg agaaggagag 1100  
 ttcttccgat gcaggttcag tcaagggaga caccattaca coagctatac 1150  
 tcagcggcct tcagcaagca gaaactgcag agtgccccta ccaagaagcc 1200  
 agcccttccc tttggagatc tgcccatggg ataccaacat ctgcataccc 1250  
 agctccagta tgagtgcac tcaccttct accgcgcct gggcagcagc 1300  
 aggaggacat gtctgaggac tgggaagtgg agtggcgagg caccatcctg 1350  
 catccctatc tgccggaaaa ttgagaacat cactgctcca aagacccaag 1400  
 ggttgctctg gccgtggcag gcagccatct acaggaggac cagcgggggtg 1450  
 catgacggca gccacacaa gggagcgtgg ttctagtct gcagcggtcg 1500  
 cctggtgaat gagcgactg tgggtgtggc tgcccactgt gttactgacc 1550  
 tggggaaggt caccatgac aagacagcag acctgaaagt tgttttgggg 1600  
 aaattotacc gggatgatga ccgggatgag aagaccatcc agagcctaca 1650  
 gattttctgt atcattctgc atcccaacta tgaccccatc ctgcttgatg 1700  
 ctgacatgc catcctgaag ctctagaca aggcocgtat cagcaccoga 1750  
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 ggagtcacc atcactgtgg ctggctggaa tgtcctggca gacgtgagga 1850  
 gccctggcct caagaacgac aactgcgct ctgggtggt cagtgtggtg 1900  
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 tgtactgat aacatgttct gtgccagctg ggaaccact gcccttctg 2000  
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 cgagcatctc ctgagccagc ctggcatctg atgggaactg tcagctggag 2100  
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 cactccttga gaagtgttcc tgtatatccg tctgtacgtg tgtcattgag 2250

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cattgtctgt aggctgatgc cgcgtccact actaggacag ccaattggaa 2400  
gatgccaggg cttgcaagaa gtaagtttct tcaagaaga ccatatacaa 2450  
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gtctctgaac tacaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2750  
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2846

<210> 231  
<211> 720  
<212> PRT  
<213> Homo sapiens

<400> 231  
Met Glu Leu Gly Cys Trp Thr Gln Leu Gly Leu Thr Phe Leu Gln  
1 5 10 15  
Leu Leu Leu Ile Ser Ser Leu Pro Arg Glu Tyr Thr Val Ile Asn  
20 25 30  
Glu Ala Cys Pro Gly Ala Glu Trp Asn Ile Met Cys Arg Glu Cys  
35 40 45  
Cys Glu Tyr Asp Gln Ile Glu Cys Val Cys Pro Gly Lys Arg Glu  
50 55 60  
Val Val Gly Tyr Thr Ile Pro Cys Cys Arg Asn Glu Glu Asn Glu  
65 70 75  
Cys Asp Ser Cys Leu Ile His Pro Gly Cys Thr Ile Phe Glu Asn  
80 85 90  
Cys Lys Ser Cys Arg Asn Gly Ser Trp Gly Gly Thr Leu Asp Asp  
95 100 105  
Phe Tyr Val Lys Gly Phe Tyr Cys Ala Glu Cys Arg Ala Gly Trp  
110 115 120  
Tyr Gly Gly Asp Cys Met Arg Cys Gly Gln Val Leu Arg Ala Pro  
125 130 135  
Lys Gly Gln Ile Leu Leu Glu Ser Tyr Pro Leu Asn Ala His Cys  
140 145 150  
Glu Trp Thr Ile His Ala Lys Pro Gly Phe Val Ile Gln Leu Arg  
155 160 165

Phe Val Met Leu Ser Leu Glu Phe Asp Tyr Met Cys Gln Tyr Asp  
 170 175 180  
 Tyr Val Glu Val Arg Asp Gly Asp Asn Arg Asp Gly Gln Ile Ile  
 185 190 195  
 Lys Arg Val Cys Gly Asn Glu Arg Pro Ala Pro Ile Gln Ser Ile  
 200 205 210  
 Gly Ser Ser Leu His Val Leu Phe His Ser Asp Gly Ser Lys Asn  
 215 220 225  
 Phe Asp Gly Phe His Ala Ile Tyr Glu Glu Ile Thr Ala Cys Ser  
 230 235 240  
 Ser Ser Pro Cys Phe His Asp Gly Thr Cys Val Leu Asp Lys Ala  
 245 250 255  
 Gly Ser Tyr Lys Cys Ala Cys Leu Ala Gly Tyr Thr Gly Gln Arg  
 260 265 270  
 Cys Glu Asn Leu Leu Glu Glu Arg Asn Cys Ser Asp Pro Gly Gly  
 275 280 285  
 Pro Val Asn Gly Tyr Gln Lys Ile Thr Gly Gly Pro Gly Leu Ile  
 290 295 300  
 Asn Gly Arg His Ala Lys Ile Gly Thr Val Val Ser Phe Phe Cys  
 305 310 315  
 Asn Asn Ser Tyr Val Leu Ser Gly Asn Glu Lys Arg Thr Cys Gln  
 320 325 330  
 Gln Asn Gly Glu Trp Ser Gly Lys Gln Pro Ile Cys Ile Lys Ala  
 335 340 345  
 Cys Arg Glu Pro Lys Ile Ser Asp Leu Val Arg Arg Arg Val Leu  
 350 355 360  
 Pro Met Gln Val Gln Ser Arg Glu Thr Pro Leu His Gln Leu Tyr  
 365 370 375  
 Ser Ala Ala Phe Ser Lys Gln Lys Leu Gln Ser Ala Pro Thr Lys  
 380 385 390  
 Lys Pro Ala Leu Pro Phe Gly Asp Leu Pro Met Gly Tyr Gln His  
 395 400 405  
 Leu His Thr Gln Leu Gln Tyr Glu Cys Ile Ser Pro Phe Tyr Arg  
 410 415 420  
 Arg Leu Gly Ser Ser Arg Arg Thr Cys Leu Arg Thr Gly Lys Trp  
 425 430 435  
 Ser Gly Arg Ala Pro Ser Cys Ile Pro Ile Cys Gly Lys Ile Glu  
 440 445 450  
 Asn Ile Thr Ala Pro Lys Thr Gln Gly Leu Arg Trp Pro Trp Gln  
 455 460 465  
 Ala Ala Ile Tyr Arg Arg Thr Ser Gly Val His Asp Gly Ser Leu  
 470 475 480

His Lys Gly Ala	Trp Phe Leu Val Cys Ser Gly Ala Leu Val Asn	485	490	495
Glu Arg Thr Val	Val Val Ala Ala His Cys Val Thr Asp Leu Gly	500	505	510
Lys Val Thr Met	Ile Lys Thr Ala Asp Leu Lys Val Val Leu Gly	515	520	525
Lys Phe Tyr Arg	Asp Asp Asp Arg Asp Glu Lys Thr Ile Gln Ser	530	535	540
Leu Gln Ile Ser	Ala Ile Ile Leu His Pro Asn Tyr Asp Pro Ile	545	550	555
Leu Leu Asp Ala	Asp Ile Ala Ile Leu Lys Leu Leu Asp Lys Ala	560	565	570
Arg Ile Ser Thr	Arg Val Gln Pro Ile Cys Leu Ala Ala Ser Arg	575	580	585
Asp Leu Ser Thr	Ser Phe Gln Glu Ser His Ile Thr Val Ala Gly	590	595	600
Trp Asn Val Leu	Ala Asp Val Arg Ser Pro Gly Phe Lys Asn Asp	605	610	615
Thr Leu Arg Ser	Gly Val Val Ser Val Val Asp Ser Leu Leu Cys	620	625	630
Glu Glu Gln His	Glu Asp His Gly Ile Pro Val Ser Val Thr Asp	635	640	645
Asn Met Phe Cys	Ala Ser Trp Glu Pro Thr Ala Pro Ser Asp Ile	650	655	660
Cys Thr Ala Glu	Thr Gly Gly Ile Ala Ala Val Ser Phe Pro Gly	665	670	675
Arg Ala Ser Pro	Glu Pro Arg Trp His Leu Met Gly Leu Val Ser	680	685	690
Trp Ser Tyr Asp	Lys Thr Cys Ser His Arg Leu Ser Thr Ala Phe	695	700	705
Thr Lys Val Leu	Pro Phe Lys Asp Trp Ile Glu Arg Asn Met Lys	710	715	720

<210> 232

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

aggttcgtga tggagacaac cgcg 24

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 233  
tgtcaaggac gcactgccgt catg 24

<210> 234  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 234  
tggccagatc atcaagcggtg tctgtggcaa cgagcggcca gctcctatcc 50

<210> 235  
<211> 1964  
<212> DNA  
<213> Homo sapiens

<400> 235  
accaggcatt gtatcttcag ttgtcatcaa gtgcgaatc agattggaaa 50  
agctcaactt gaagctttct tgctgcagt gaagcagaga gatagatatt 100  
attcacgtaa taaaaaacat gggcttcaac ctgactttcc accttctcta 150  
caaattccga ttactgttgc tgttgacttt gtgctgaca gtgggtgggt 200  
gggccaccag taactacttc gtgggtgcca tccaagatg tcctaaagca 250  
aaggagtcca tggctaattt ccataagacc ctcatcttgg ggaaggga 300  
aactctgact aatgaagcat ccacgaagaa ggtagaactt gacaactgtc 350  
cttctgtgtc tcttacctc agaggccaga gcaagctcat tttcaaacca 400  
gatctcaatt tgggaagagt acaggcagaa aatcccaaag tgtccagagg 450  
cgggtatogc cctcaggaat gtaaagcttt acagagggtc gccatcctcg 500  
ttccccaccg gaacagagag aaacacctga tgtacctgct ggaacatctg 550  
catcccttcc tgcagaggca gcagctggat tatggcatct acgtcatcca 600  
ccaggctgaa ggtaaaaagt ttaatcgagc caaactcttg aatgtgggct 650  
atctagaagc cctcaaggaa gaaaattggg actgctttat attccacgat 700  
gtggacctgg tacccgagaa tgactttaac ctttacaagt gtgaggagca 750  
tcccaagcat ctggtggttg gcaggaacag cactgggtac aggttacggt 800  
acagtggata ttttgggggt gttactgcc taagcagaga cgagtttttc 850  
aagggtgaat gattctctaa caactactgg ggaatggggag gcgaagacga 900  
tgacctcaga ctacgggttg agctccaaag aatgaaaatt tcccgcccc 950  
tgctgaagt gggtaaatat acaatggtct tccacactag agacaaaggc 1000

aatgaggtga acgcagaacg gatgaagctc ttacaccaag tgtcacgagt 1050  
 ctggagaaca gatgggttga gtagttgttc ttataaatta gtatctgttg 1100  
 aacacaatoc tttatatatc aacatcacag tggatttctg gtttggtgca 1150  
 tgacctgga tcttttgggtg atgtttggaa gaactgatto tttggttgca 1200  
 ataattttgg cctagagact tcaaatagta gcacacatta agaacctgtt 1250  
 acagctcatt gttgagctga atttttctt tttgtatttt cttagcagag 1300  
 ctctcgttga tgtagagtat aaaacagttg taacaagaca gctttcttag 1350  
 tcattttgat catgagggtt aaatattgta atatggatac ttgaaggact 1400  
 ttatataaaa ggatgactca aaggataaaa tgaacgctat ttgaggactc 1450  
 tggttgaagg agatttat tt aaatttgaag taatatatta tgggataaaa 1500  
 ggccacagga aataagactg ctgaatgtct gagagaacca gagttgttct 1550  
 cgtccaaggt agaaaggtag gaagatacaa tactgttatt cattttatcct 1600  
 gtacaatcat ctgtgaagtg gtgtgtgcag gtgagaaggc gtcacaaaaa 1650  
 gaggggagaa aaggcgacga atcaggacac agtgaacttg ggaatgaaga 1700  
 ggtagcagga gggtggagtg tcggctgcaa aggcagcagt agctgagctg 1750  
 gttgcagtg ctgatagcct tcaggggagg acctgccag gtatgccttc 1800  
 cagtgatgcc caccagagaa tacattctct attagttttt aaagagtttt 1850  
 tgtaaaatga ttttgtacaa gtaggatatg aattagcagt ttacaagttt 1900  
 acatattaac taataataaa tatgtctatc aaatacctct gtagtaaaa 1950  
 gtgaaaaagc aaaa 1964

<210> 236  
 <211> 344  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> Signal peptide  
 <222> 1-27  
 <223> Signal peptide

<220>  
 <221> N-glycosylation sites  
 <222> 4-7, 220-223, 335-338  
 <223> N-glycosylation sites

<220>  
 <221> Xylose isomerase proteins  
 <222> 191-201  
 <223> Xylose isomerase proteins

<400> 236  
 Met Gly Phe Asn Leu Thr Phe His Leu Ser Tyr Lys Phe Arg Leu  
 1 5 10 15



Leu	Leu	Leu	Leu	Thr	Leu	Cys	Leu	Thr	Val	Val	Gly	Trp	Ala	Thr	
				20					25					30	
Ser	Asn	Tyr	Phe	Val	Gly	Ala	Ile	Gln	Glu	Ile	Pro	Lys	Ala	Lys	
				35					40					45	
Glu	Phe	Met	Ala	Asn	Phe	His	Lys	Thr	Leu	Ile	Leu	Gly	Lys	Gly	
				50					55					60	
Lys	Thr	Leu	Thr	Asn	Glu	Ala	Ser	Thr	Lys	Lys	Val	Glu	Leu	Asp	
				65					70					75	
Asn	Cys	Pro	Ser	Val	Ser	Pro	Tyr	Leu	Arg	Gly	Gln	Ser	Lys	Leu	
				80					85					90	
Ile	Phe	Lys	Pro	Asp	Leu	Thr	Leu	Glu	Glu	Val	Gln	Ala	Glu	Asn	
				95					100					105	
Pro	Lys	Val	Ser	Arg	Gly	Arg	Tyr	Arg	Pro	Gln	Glu	Cys	Lys	Ala	
				110					115					120	
Leu	Gln	Arg	Val	Ala	Ile	Leu	Val	Pro	His	Arg	Asn	Arg	Glu	Lys	
				125					130					135	
His	Leu	Met	Tyr	Leu	Leu	Glu	His	Leu	His	Pro	Phe	Leu	Gln	Arg	
				140					145					150	
Gln	Gln	Leu	Asp	Tyr	Gly	Ile	Tyr	Val	Ile	His	Gln	Ala	Glu	Gly	
				155					160					165	
Lys	lys	Phe	Asn	Arg	Ala	Lys	Leu	Leu	Asn	Val	Gly	Tyr	Leu	Glu	
				170					175					180	
Ala	Leu	Lys	Glu	Glu	Asn	Trp	Asp	Cys	Phe	Ile	Phe	His	Asp	Val	
				185					190					195	
Asp	Leu	Val	Pro	Glu	Asn	Asp	Phe	Asn	Leu	Tyr	Lys	Cys	Glu	Glu	
				200					205					210	
His	Pro	Lys	His	Leu	Val	Val	Gly	Arg	Asn	Ser	Thr	Gly	Tyr	Arg	
				215					220					225	
Leu	Arg	Tyr	Ser	Gly	Tyr	Phe	Gly	Gly	Val	Thr	Ala	Leu	Ser	Arg	
				230					235					240	
Glu	Gln	Phe	Phe	Lys	Val	Asn	Gly	Phe	Ser	Asn	Asn	Tyr	Trp	Gly	
				245					250					255	
Trp	Gly	Gly	Glu	Asp	Asp	Asp	Leu	Arg	Leu	Arg	Val	Glu	Leu	Gln	
				260					265					270	
Arg	Met	Lys	Ile	Ser	Arg	Pro	Leu	Pro	Glu	Val	Gly	Lys	Tyr	Thr	
				275					280					285	
Met	Val	Phe	His	Thr	Arg	Asp	Lys	Gly	Asn	Glu	Val	Asn	Ala	Glu	
				290					295					300	
Arg	Met	Lys	Leu	Leu	His	Gln	Val	Ser	Arg	Val	Trp	Arg	Thr	Asp	
				305					310					315	
Gly	Leu	Ser	Ser	Cys	Ser	Tyr	Lys	Leu	Val	Ser	Val	Glu	His	Asn	
				320					325					330	

Pro Leu Tyr Ile Asn Ile Thr Val Asp Phe Trp Phe Gly Ala  
335 340

<210> 237  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 237  
ccttacctca gaggccagag caagc 25

<210> 238  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 238  
gagcttcacg cgttctgcgt tcacc 25

<210> 239  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 239  
caggaatgta aagctttaca gagggctgcc atcctcgttc cccacc 46

<210> 240  
<211> 2567  
<212> DNA  
<213> Homo sapiens

<400> 240  
cgtgggcccgg ggtcgcgcag cgggctgtgg gcgcgcccg aggagcgacc 50  
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tctcccgcct cgggcccccgc aatggcccag gcagtgtggt cgcgcctcgg 150  
ccgcatactc tggcttgccct gcctcctgcc ctgggccccg gcagggggtg 200  
ccgcaggcct gtatgaactc aatctcacca ccgatagccc tgccaccacg 250  
ggagcgggtg tgaccatctc ggccagcctg gtggccaagg acaacggcgag 300  
cctggccctg ccccgctgacg cccacctcta ccgcttccac tggatccaca 350  
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cgtgtggtcg gccacgtgcc cggggaattc ccggtctctg tetgggtcac 450  
tgccgctgac tgctggatgt gccagcctgt ggccaggggc tttgtggtcc 500  
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tcctaccct ggcccagctc ctatctact aagaccgtcc tgaaagtctc 600  
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 acagctggga ctctggggac gggaccaga tggtagctga agactccgtg 700  
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 ggtggcggag tgggaagagg tggagccgga tgccacgagg gctgtgaagc 800  
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 cgtgaccttg aacttctcgg ggagccctcc tctgactgtg tgetgggctc 950  
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 gtggccagca cagcgtacaa cctgaccac accttcagg accctgggga 1050  
 ctactgcttc agcatccggg ccgagaatat catcagcaag acacatcagt 1100  
 accacaagat ccaggtgtgg ccctccagaa tccagccggc tgtcttctgt 1150  
 ttccatgtg ctacacttat cactgtgatg ttggccttca tcatgtacat 1200  
 gacctcgagg aatgccactc agcaaaagga catggtggag aaccgggagc 1250  
 caccctctgg ggtcagggtc tgetgccaga tgtgctgtgg gccctttctg 1300  
 ctggagactc catotgagta cctggaaatt gttcgtgaga accacgggct 1350  
 gctcccgccc ctctataagt ctgtcaaac ttacaccgtg tgagcactcc 1400  
 cctcccccac ccatctcag tgttaactga ctgctgactt ggagtttcca 1450  
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 cctccctctc tgtcacccct gacccagcc attcacccat ctgtacagtc 1600  
 cagccactga cataagcccc actcgggttac caccctcttg accccctacc 1650  
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 ctctagggtg ggctgtgctg cccactgcc attcctctca tattggcaca 1750  
 tctgtgttcc attgggggtt ctacgtttcc tccccagac agccctacct 1800  
 gtgccagaga gctagaaga aggtcataaa ggggtaaaaa tccataacta 1850  
 aaggtgttac acatagatgg gcacactcac agagagaagt gtgcattgac 1900  
 acacaccaca cacacacaca cacacacaca cacagaaata taaacacatg 1950  
 cgtcacattg gcatttcaga tgatcagctc tgtatctggt taagtccggt 2000  
 gctgggagtgc accctgcact agagctgaaa ggaaatttga cctccaagca 2050  
 gccctgacag gttctggggc cggggccctcc ctttctgctt tgtctctgca 2100  
 gttcttgcgc cctttataag gcatactag tccctgctgg ctggcagggg 2150

cctggatggg gggcaggact aatactgagt gattgcagag tgctttataa 2200  
 atatcacctt attttatcga aacccatctg tgaactttc actgaggaaa 2250  
 aggccttgca gcggtagaag aggttgagtc aaggccgggc gcggtggctc 2300  
 acgcctgtaa tcccagcact ttgggaggcc gaggcgggtg gatcacgaga 2350  
 tcaggagatc gagaccacc ttgctaacac ggtgaaaccc cgtctctact 2400  
 aaaaaaatac aaaaagttag ccgggcgtgg tgggtgggtg ctgtagtccc 2450  
 agctactcgg gaggtcgagg caggagaatg gtgcgaaccc gggaggcgga 2500  
 gcttgcaagt agcccagatg gcgcoactgc actccagcct gaggacaga 2550  
 gcgagactct gtctcca 2567

<210> 241  
 <211> 423  
 <212> PRT  
 <213> Homo sapiens

<400> 241  
 Met Ala Gln Ala Val Trp Ser Arg Leu Gly Arg Ile Leu Trp Leu  
 1 5 10 15  
 Ala Cys Leu Leu Pro Trp Ala Pro Ala Gly Val Ala Ala Gly Leu  
 20 25 30  
 Tyr Glu Leu Asn Leu Thr Thr Asp Ser Pro Ala Thr Thr Gly Ala  
 35 40 45  
 Val Val Thr Ile Ser Ala Ser Leu Val Ala Lys Asp Asn Gly Ser  
 50 55 60  
 Leu Ala Leu Pro Ala Asp Ala His Leu Tyr Arg Phe His Trp Ile  
 65 70 75  
 His Thr Pro Leu Val Leu Thr Gly Lys Met Glu Lys Gly Leu Ser  
 80 85 90  
 Ser Thr Ile Arg Val Val Gly His Val Pro Gly Glu Phe Pro Val  
 95 100 105  
 Ser Val Trp Val Thr Ala Ala Asp Cys Trp Met Cys Gln Pro Val  
 110 115 120  
 Ala Arg Gly Phe Val Val Leu Pro Ile Thr Glu Phe Leu Val Gly  
 125 130 135  
 Asp Leu Val Val Thr Gln Asn Thr Ser Leu Pro Trp Pro Ser Ser  
 140 145 150  
 Tyr Leu Thr Lys Thr Val Leu Lys Val Ser Phe Leu Leu His Asp  
 155 160 165  
 Pro Ser Asn Phe Leu Lys Thr Ala Leu Phe Leu Tyr Ser Trp Asp  
 170 175 180  
 Phe Gly Asp Gly Thr Gln Met Val Thr Glu Asp Ser Val Val Tyr  
 185 190 195

Tyr Asn Tyr Ser Ile Ile Gly Thr Phe Thr Val Lys Leu Lys Val  
 200 205 210  
 Val Ala Glu Trp Glu Glu Val Glu Pro Asp Ala Thr Arg Ala Val  
 215 220 225  
 Lys Gln Lys Thr Gly Asp Phe Ser Ala Ser Leu Lys Leu Gln Glu  
 230 235 240  
 Thr Leu Arg Gly Ile Gln Val Leu Gly Pro Thr Leu Ile Gln Thr  
 245 250 255  
 Phe Gln Lys Met Thr Val Thr Leu Asn Phe Leu Gly Ser Pro Pro  
 260 265 270  
 Leu Thr Val Cys Trp Arg Leu Lys Pro Glu Cys Leu Pro Leu Glu  
 275 280 285  
 Glu Gly Glu Cys His Pro Val Ser Val Ala Ser Thr Ala Tyr Asn  
 290 295 300  
 Leu Thr His Thr Phe Arg Asp Pro Gly Asp Tyr Cys Phe Ser Ile  
 305 310 315  
 Arg Ala Glu Asn Ile Ile Ser Lys Thr His Gln Tyr His Lys Ile  
 320 325 330  
 Gln Val Trp Pro Ser Arg Ile Gln Pro Ala Val Phe Ala Phe Pro  
 335 340 345  
 Cys Ala Thr Leu Ile Thr Val Met Leu Ala Phe Ile Met Tyr Met  
 350 355 360  
 Thr Leu Arg Asn Ala Thr Gln Gln Lys Asp Met Val Glu Asn Pro  
 365 370 375  
 Glu Pro Pro Ser Gly Val Arg Cys Cys Cys Gln Met Cys Cys Gly  
 380 385 390  
 Pro Phe Leu Leu Glu Thr Pro Ser Glu Tyr Leu Glu Ile Val Arg  
 395 400 405  
 Glu Asn His Gly Leu Leu Pro Pro Leu Tyr Lys Ser Val Lys Thr  
 410 415 420  
 Tyr Thr Val

<210> 242  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 242  
 catttcotta ccttgacc agctcc 26  
  
 <210> 243  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 243  
gaaaggccca cagcacatct ggcag 25

<210> 244  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 244  
ccacgaccg agcaacttc toaagaccga ctgtttctc tacagc 46

<210> 245  
<211> 485  
<212> DNA  
<213> Homo sapiens

<400> 245  
gtccaagacc cagcagtggg acagccagac agacggcacg atggcactga 50  
gtccccagat ctgggcccgt tgcctcctgc tctcctcct cctcgccagc 100  
ctgaccagtg gctctgtttt cccacaacag acgggacaac ttgcagagct 150  
gcaaccccag gacagagctg gagccagggc cagctggatg cccatgttcc 200  
agaggcgaag gaggcgagac acccacttcc ccatctgcat tttctgctgc 250  
ggctgctgtc atcgatcaaa gtgtgggatg tgctgcaaga cgtagaacct 300  
acctgcctg cccccgtccc ctcccttctc tatttatctc tgctgcccc 350  
gaacataggt cttggaataa aatggctggt tctttgttt tccaaaaaaa 400  
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450  
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 485

<210> 246  
<211> 84  
<212> PRT  
<213> Homo sapiens

<400> 246  
Met Ala Leu Ser Ser Gln Ile Trp Ala Ala Cys Leu Leu Leu Leu  
1 5 10 15  
Leu Leu Leu Ala Ser Leu Thr Ser Gly Ser Val Phe Pro Gln Gln  
20 25 30  
Thr Gly Gln Leu Ala Glu Leu Gln Pro Gln Asp Arg Ala Gly Ala  
35 40 45  
Arg Ala Ser Trp Met Pro Met Phe Gln Arg Arg Arg Arg Asp  
50 55 60  
Thr His Phe Pro Ile Cys Ile Phe Cys Cys Gly Cys Cys His Arg  
65 70 75

Ser Lys Cys Gly Met Cys Cys Lys Thr

80

<210> 247  
<211> 2359  
<212> DNA  
<213> Homo sapiens

<400> 247  
ctgtcaggaa ggaccatctg aaggctgcaa ttgtttotta gggaggcagg 50  
tgctggcctg gcttggatct tccaccatgt tctgttggct gccctttgat 100  
agcctgattg tcaaccttct gggcatctcc ctgactgtcc tcttcacctc 150  
ccttctcgtt ttcacatag tgccagccat ttttgagtc tcttttggtg 200  
tccgcaaact ctacatgaaa agtctgttaa aaatctttgc gtgggctacc 250  
ttgagaattg agcgaggagc caaggagaag aaccaccagc tttaacaagg 300  
ctacaccaac ggaatcattg caaaggatcc cacttcacta gaagaagaga 350  
tcaaagagat tcgtcgaagt ggtagtagta aggctctgga caacactcca 400  
gagttcagag cctctgacat ttctactttt tgccggaaa gaaaggagac 450  
cattatggat gatgagggtg caaagagatt ctcagcagaa gaactggagt 500  
cctggaaact gctgagcaga accaattata acttcagta catcagcctt 550  
cggctcacgg tctctgtggg gttaggagtg ctgattcggg actgctttct 600  
gctgccgctc aggatagcac tggctttcac agggattagc cttctggttg 650  
tgggcacaa cgtgtgtgga tacttgccaa atgggaggtt taaggaaatt 700  
atgagtaaac atgttcactt aatgtgttac cggatctgcg tgcgagcgct 750  
gacagccatc atcaoctacc atgacaggga aaacagacca agaaaattgt 800  
gcatctgtgt ggccaatcat acctcaccca tcgatgtgat catcttggcc 850  
agcgtaggct attatgccat ggtgggtcaa gtgcacgggg gactcatggg 900  
tgtgattcag agagccatgg tgaaggcctg cccacacgct tggtttgagc 950  
gctcggaagt gaaggatcgc cacctggttg ctaagagact gactgaacat 1000  
gtgcaagata aaagcaagct gcctatcctc atcttccag aaggaaacct 1050  
catcaataat acatcgggtg tgatgttcaa aaagggaagt tttgaaattg 1100  
gagccacagt ttacctgtt gctatcaagt atgacctca atttggcgat 1150  
gccttctgga acagcagcaa atacgggatg gtgacgtacc tgctgcgaat 1200  
gatgaccagc tgggcattg tctgcagcgt gtggtacctg cctcccatga 1250  
ctagagaggc agatgaagat gctgtccagt ttgcgaatat ggtgaaatct 1300  
gccattgcca ggcaggaggg acttgtggac ctgctgtggg atgggggcct 1350

gaagagggag aaggtgaagg acacgttcaa ggaggagcag cagaagctgt 1400  
 acagcaagat gatogtgggg aaccacaagg acaggagccg ctctgagcc 1450  
 tgcctccagc tggtctgggg caccgtgcgg ggtgccaaag ggtccagagc 1500  
 tggagtgtgc gccgccgcc cactgtctgt gtctttcca gactccaggg 1550  
 ctccccgggc tgctctggat ccaggagctc cggttttgc cgagccgag 1600  
 cgggatccct gtgcaccgg cgcagcctac cttgtgtgt ctaaacggat 1650  
 gctgtgtggt gttgcgaccc aggacgagat gccttgtttc tttacaata 1700  
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 gcgggtctgag tggttgggga gatgtggcca tggctctgtg ctagagatgg 1800  
 cggtagaaga gtctgttatg caagcccggtg tggcagggat gtgtctgggg 1850  
 cggccaccgc ctctccagga aaggcacagc tgaggcactg tggctggcct 1900  
 cggcctcaac atcgccccca gccttgagc tctgcagaca tgataggaag 1950  
 gaaactgtca tctgcagggg ctttcagcaa aatgaagggt tagattttta 2000  
 tgctgtctgt gatgggggta ctaaaggag gggaagaggc caggtgggcc 2050  
 gctgactggg ccatggggag aacgtgtgtt cgtactccag gctaaccctg 2100  
 aactcccat gtgatgcgcg cttgttgaa tgtgtgtct gggttccca 2150  
 tctgtaatat gagtccgggg gaatgtgtgt gattcctacc tcacagggt 2200  
 gttgtgggga ttaaagtgt gcgggtgagt gaaggacaca tcacgttcag 2250  
 tgtttcaagt acaggccac aaaacggggc acggcaggcc tgagctcaga 2300  
 gctgtgcac tgggttttg attgttctt gtgagtaaat aaaactggct 2350  
 ggtgaatga 2359

<210> 248  
 <211> 456  
 <212> FRT  
 <213> Homo sapiens

<400> 248  
 Met Phe Leu Leu Leu Pro Phe Asp Ser Leu Ile Val Asn Leu Leu  
 1 5 10 15  
 Gly Ile Ser Leu Thr Val Leu Phe Thr Leu Leu Leu Val Phe Ile  
 20 25 30  
 Ile Val Pro Ala Ile Phe Gly Val Ser Phe Gly Ile Arg Lys Leu  
 35 40 45  
 Tyr Met Lys Ser Leu Leu Lys Ile Phe Ala Trp Ala Thr Leu Arg  
 50 55 60  
 Met Glu Arg Gly Ala Lys Glu Lys Asn His Gln Leu Tyr Lys Pro  
 65 70 75



Tyr Thr Asn Gly	Ile 80	Ile Ala Lys Asp	Pro 85	Thr Ser Leu Glu	Glu 90
Glu Ile Lys Glu	Ile 95	Arg Arg Ser Gly	Ser 100	Ser Lys Ala Leu	Asp 105
Asn Thr Pro Glu	Phe 110	Glu Leu Ser Asp	Ile 115	Phe Tyr Phe Cys	Arg 120
Lys Gly Met Glu	Thr 125	Ile Met Asp Asp	Glu 130	Val Thr Lys Arg	Phe 135
Ser Ala Glu Glu	Leu 140	Glu Ser Trp Asn	Leu 145	Leu Ser Arg Thr	Asn 150
Tyr Asn Phe Gln	Tyr 155	Ile Ser Leu Arg	Leu 160	Thr Val Leu Trp	Gly 165
Leu Gly Val Leu	Ile 170	Arg Tyr Cys Phe	Leu 175	Leu Pro Leu Arg	Ile 180
Ala Leu Ala Phe	Thr 185	Gly Ile Ser Leu	Leu 190	Val Val Gly Thr	Thr 195
Val Val Gly Tyr	Leu 200	Pro Asn Gly Arg	Phe 205	Lys Glu Phe Met	Ser 210
Lys His Val His	Leu 215	Met Cys Tyr Arg	Ile 220	Cys Val Arg Ala	Leu 225
Thr Ala Ile Ile	Thr 230	Tyr His Asp Arg	Glu 235	Asn Arg Pro Arg	Asn 240
Gly Gly Ile Cys	Val 245	Ala Asn His Thr	Ser 250	Pro Ile Asp Val	Ile 255
Ile Leu Ala Ser	Asp 260	Gly Tyr Tyr Ala	Met 265	Val Gly Gln Val	His 270
Gly Gly Leu Met	Gly 275	Val Ile Gln Arg	Ala 280	Met Val Lys Ala	Cys 285
Pro His Val Trp	Phe 290	Glu Arg Ser Glu	Val 295	Lys Asp Arg His	Leu 300
Val Ala Lys Arg	Leu 305	Thr Glu His Val	Gln 310	Asp Lys Ser Lys	Leu 315
Pro Ile Leu Ile	Phe 320	Pro Glu Gly Thr	Cys 325	Ile Asn Asn Thr	Ser 330
Val Met Met Phe	Lys 335	Lys Gly Ser Phe	Glu 340	Ile Gly Ala Thr	Val 345
Tyr Pro Val Ala	Ile 350	Lys Tyr Asp Pro	Gln 355	Phe Gly Asp Ala	Phe 360
Trp Asn Ser Ser	Lys 365	Tyr Gly Met Val	Thr 370	Tyr Leu Leu Arg	Met 375
Met Thr Ser Trp	Ala 380	Ile Val Cys Ser	Val 385	Trp Tyr Leu Pro	Pro 390

Met Thr Arg Glu Ala Asp Glu Asp Ala Val Gln Phe Ala Asn Arg  
 395 400  
 Val Lys Ser Ala Ile Ala Arg Gln Gly Gly Leu Val Asp Leu Leu  
 410 415 420  
 Trp Asp Gly Gly Leu Lys Arg Glu Lys Val Lys Asp Thr Phe Lys  
 425 430 435  
 Glu Glu Gln Gln Lys Leu Tyr Ser Lys Met Ile Val Gly Asn His  
 440 445 450  
 Lys Asp Arg Ser Arg Ser  
 455

<210> 249  
 <211> 1103  
 <212> DNA  
 <213> Homo sapiens

<400> 249  
 gccccctcgaa accaggactc cagcacctct ggtccccgcc tcacccggac 50  
 ccctggccct cagctctcct ccagggatgg cgctggcggc tttgatgatc 100  
 gccctcggca gcctcggcct ccacacctgg caggcccagg ctgttcccac 150  
 catcctgccc ctgggcctgg ctccagacac ctttgacgat acctatgttg 200  
 gttgtgcaga ggagatggag gagaaggcag cccccctgct aaaggaggaa 250  
 atggcccacc atgccctgct gcgggaatcc tgggaggcag ccaggagac 300  
 ctgggaggac aagcgtcag ggcttacctt gccccctggc tcaaaagccc 350  
 agaatggaat agccattatg gtctacacca actcatcgaa caccctgtac 400  
 tgggagttga atcaggccgt gcggacgggc ggaggctccc gggagctcta 450  
 catgaggcac ttcccttca aggccctgca tttctacctg atccgggccc 500  
 tgcagctgct gcgaggcagt gggggctgca gcaggggacc tggggagggtg 550  
 gtgttcocag gtgtgggcag ccttcgcttt gaacccaaga ggctggggga 600  
 ctctgtccgc ttgggccagt ttgectccag ctccctggat aaggcagtgg 650  
 cccacagatt tggggagaag aggcggggct gtgtgtctgc gccagggggtg 700  
 cagctagggt cacaatctga gggggcctcc tctctgcccc cctggaagac 750  
 tctgtctctg gccctggag agttccagct ctacagggtt gggccctgaa 800  
 agtccaacat ctgccactta ggagccctgg gaacgggtga cttcatatg 850  
 acgaagaggc acctccagca gccttgagaa gcaagaacat ggttccggac 900  
 ccagccctag cagccttctc cccaaccagg atgttggcct ggggaggcca 950  
 cagcagggtg gagggaactc tgctatgtga tggggacttc ctgggacaag 1000  
 caaggaaagt actgaggcag ccacttgatt gaacggtgtt gcaatgtgga 1050

gacatggagt tttattgagg tagctacgtg attaaatggt attgcagtgt 1100

gga 1103

<210> 250

<211> 240

<212> PRT

<213> Homo sapiens

<400> 250

Met Ala Leu Ala Ala Leu Met Ile Ala Leu Gly Ser Leu Gly Leu  
1 5 10 15

His Thr Trp Gln Ala Gln Ala Val Pro Thr Ile Leu Pro Leu Gly  
20 25 30

Leu Ala Pro Asp Thr Phe Asp Asp Thr Tyr Val Gly Cys Ala Glu  
35 40 45

Glu Met Glu Glu Lys Ala Ala Pro Leu Leu Lys Glu Glu Met Ala  
50 55 60

His His Ala Leu Leu Arg Glu Ser Trp Glu Ala Ala Gln Glu Thr  
65 70 75

Trp Glu Asp Lys Arg Arg Gly Leu Thr Leu Pro Pro Gly Phe Lys  
80 85 90

Ala Gln Asn Gly Ile Ala Ile Met Val Tyr Thr Asn Ser Ser Asn  
95 100 105

Thr Leu Tyr Trp Glu Leu Asn Gln Ala Val Arg Thr Gly Gly Gly  
110 115 120

Ser Arg Glu Leu Tyr Met Arg His Phe Pro Phe Lys Ala Leu His  
125 130 135

Phe Tyr Leu Ile Arg Ala Leu Gln Leu Leu Arg Gly Ser Gly Gly  
140 145 150

Cys Ser Arg Gly Pro Gly Glu Val Val Phe Arg Gly Val Gly Ser  
155 160 165

Leu Arg Phe Glu Pro Lys Arg Leu Gly Asp Ser Val Arg Leu Gly  
170 175 180

Gln Phe Ala Ser Ser Ser Leu Asp Lys Ala Val Ala His Arg Phe  
185 190 195

Gly Glu Lys Arg Arg Gly Cys Val Ser Ala Pro Gly Val Gln Leu  
200 205 210

Gly Ser Gln Ser Glu Gly Ala Ser Ser Leu Pro Pro Trp Lys Thr  
215 220 225

Leu Leu Leu Ala Pro Gly Glu Phe Gln Leu Ser Gly Val Gly Pro  
230 235 240

<210> 251

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 251

ccaccacctg gaggtctctgc agtggggcag gaactccatc cggcagattg 50

<210> 252

<211> 1076

<212> DNA

<213> Homo sapiens

<400> 252

gtggcttcac ttacagtggc gacttccaga gagcaatatg gctgggtccc 50

caacatgcct caccctcatc tatatccttt ggcagctcac agggtcagca 100

gcctctggac ccgtagaaga gctgggtcggg tccgttggg gggccgtgac 150

tttcccctg aagtccaaag taaagcaagt tgactctatt gtctggacct 200

tcaacacaac ccctcttgct accatacagc cagaaggggg cactatcata 250

gtgacccaaa atcgtaatag ggagagagta gacttccag atggaggcta 300

ctccctgaag ctacagaaa tgaagaagaa tgactcaggg atctactatg 350

tggggatata cagctcatca ctccagcagc cctccaccca ggagtactgt 400

ctgcatgtct acgagcacct gtcaaagcct aaagtcacca tgggtctgca 450

gagcaataag aatggcacct gtgtgaccaa tctgacatgc tgcattgaac 500

atgggggaaga ggatgtgatt tatacctgga aggcctctgg gcaagcagcc 550

aatgagtcac ataattgggtc catcctcccc atctctctgga gatggggaga 600

aagtgatatg accttcattc gcgttgccag gaacctgtgc agcagaaaact 650

tctcaagccc catccttgcc aggaagctct gtgaagggtc tgctgatgac 700

ccagattcct ccatgttcct cctgtgtctc ctgttggtgc cctctctgct 750

cagtcctctt gtactggggc tatttctttg gtttctgaag agagagagac 800

aagaagagta cattgaagag aagaagagag tggacatttg tcgggaaact 850

cctaacatat gcccccattc tggagagaac acagagtacg acacaatccc 900

tcacactaat agaacaatcc taaaggaaga tccagcaaat acggtttact 950

ccactgtgga aataccgaaa aagatggaaa atccccactc actgctcacg 1000

atgccagaca caccaaggct atttgctat gagaatgta tctagacagc 1050

agtgcactcc cctaagcttc tgcctca 1076

<210> 253

<211> 335

<212> PRT

<213> Homo sapiens

<400> 253

Met Ala Gly Ser Pro Thr Cys Leu Thr Leu Ile Tyr Ile Leu Trp

1	5	10	15
Gln Leu Thr Gly	Ser Ala Ala Ser Gly	Pro Val Lys Glu Leu Val	20 25 30
Gly Ser Val Gly	Gly Ala Val Thr Phe	Pro Leu Lys Ser Lys Val	35 40 45
Lys Gln Val Asp	Ser Ile Val Trp Thr	Phe Asn Thr Thr Pro Leu	50 55 60
Val Thr Ile Gln	Pro Glu Gly Gly Thr	Ile Ile Val Thr Gln Asn	65 70 75
Arg Asn Arg Glu	Arg Val Asp Phe Pro	Asp Gly Gly Tyr Ser Leu	80 85 90
Lys Leu Ser Lys	Leu Lys Lys Asn Asp	Ser Gly Ile Tyr Tyr Val	95 100 105
Gly Ile Tyr Ser	Ser Ser Leu Gln Gln	Pro Ser Thr Gln Glu Tyr	110 115 120
Val Leu His Val	Tyr Glu His Leu Ser	Lys Pro Lys Val Thr Met	125 130 135
Gly Leu Gln Ser	Asn Lys Asn Gly Thr	Cys Val Thr Asn Leu Thr	140 145 150
Cys Cys Met Glu	His Gly Glu Glu Asp	Val Ile Tyr Thr Trp Lys	155 160 165
Ala Leu Gly Gln	Ala Ala Asn Glu Ser	His Asn Gly Ser Ile Leu	170 175 180
Pro Ile Ser Trp	Arg Trp Gly Glu Ser	Asp Met Thr Phe Ile Cys	185 190 195
Val Ala Arg Asn	Pro Val Ser Arg Asn	Phe Ser Ser Pro Ile Leu	200 205 210
Ala Arg Lys Leu	Cys Glu Gly Ala Ala	Asp Asp Pro Asp Ser Ser	215 220 225
Met Val Leu Leu	Cys Leu Leu Leu Val	Pro Leu Leu Leu Ser Leu	230 235 240
Phe Val Leu Gly	Leu Phe Leu Trp Phe	Leu Lys Arg Glu Arg Gln	245 250 255
Glu Glu Tyr Ile	Glu Glu Lys Lys Arg	Val Asp Ile Cys Arg Glu	260 265 270
Thr Pro Asn Ile	Cys Pro His Ser Gly	Glu Asn Thr Glu Tyr Asp	275 280 285
Thr Ile Pro His	Thr Asn Arg Thr Ile	Leu Lys Glu Asp Pro Ala	290 295 300
Asn Thr Val Tyr	Ser Thr Val Glu Ile	Pro Lys Lys Met Glu Asn	305 310 315
Pro His Ser Leu	Leu Thr Met Pro Asp	Thr Pro Arg Leu Phe Ala	

Tyr Glu Asn Val Ile  
335

<210> 254  
<211> 1053  
<212> DNA  
<213> Homo sapiens

<400> 254  
ctggttcccc aacatgcctc accctcatct atataccttg gcagctcaca 50  
gggtcagcag cctctggacc cgtgaaagag ctggctcggtt ccgttggttg 100  
ggcctgact ttccccctga agtccaaagt aaagcaagtt gactctattg 150  
tctggacctt caacacaacc cctcttgta ccatcacagcc agaagggggc 200  
actatcatag tgaccacaaa tcgtaatatg gagagagtag acttcccaga 250  
tggaggctac tccttgaagc tcagcaaact gaagaagaat gactcaggga 300  
tctactatgt ggggatatac agctcatcac tccagcagcc ctccaccag 350  
gagtagctgc tgcattgtcta cgagcacctg tcaaagccta aagtcaccat 400  
gggtctgcag agcaataaga atggcacctg tgtgaccaat ctgacatgct 450  
gcatggaaca tggggaagag gatgtgattt atacctgaa ggccttggg 500  
caagcagcca atgagtccca taatgggtcc atcctcccca tctcctggag 550  
atggggagaa agtgatatga ccttcatctg cgttgccagg aacctgtca 600  
gcagaaactt ctcaagcccc atccttgcca ggaagctctg tgaaggtgct 650  
gctgatgacc cagattcctc catggtcctc ctgtgtctcc tgttggtgcc 700  
cctcctgctc agtctctttg tactggggct atttcttttg tttctgaaga 750  
gagagagaca agaagagtac attgaagaga agaagagagt ggacatttgt 800  
cgggaaactc ctaacatatg ccccatctct ggagagaaca cagagtacga 850  
cacaatccct cactaataa gaacaatcct aaaggaagat ccagcaaata 900  
cggtttactc cactgtggaa ataccgaaaa agatggaaaa tccccactca 950  
ctgtcacgca tgccagacac accaaggcta ttgcctatg agaattgtat 1000  
ctagacagca gtgcactccc ctaagtctct gctcaaaaaa aaaaaaaaaa 1050  
aaa 1053

<210> 255  
<211> 860  
<212> DNA  
<213> Homo sapiens

<400> 255  
gaaagacgtg gtcctgacag acagacaatc ctattcccta ccaaatgaa 50

gatgctgctg ctgctgtgtt tgggactgac cctagtctgt gtccatgcag 100  
 aagaagctag ttctacggga aggaacttta atgtagaaaa gattaatggg 150  
 gaatggcata ctattatcct ggctctgac aaaagagaaa agatagaaga 200  
 acatggcaac tttagacttt ttctggagca aatccatgtc ttggagaatt 250  
 ccttagttct taaagtccat actgtaagag atgaagagtg ctccgaatta 300  
 tctatggttg ctgacaaaac agaaaaggct ggtgaatatt ctgtgacgta 350  
 tgatggattc aatacattta ctatacctaa gacagactat gataactttc 400  
 ttatggctca cctcattaac gaaaaggatg gggaaacott ccagctgatg 450  
 gggctctatg gccgagaacc agatttgagt tcagacatca aggaaagggt 500  
 tgcacaacta tgtgaggagc atggaatcct tagagaaaa atcattgacc 550  
 tatccaatgc caatcgctgc ctccaggccc gagaatgaag aatggcctga 600  
 gcctccagtg ttgagtggac acttctcacc aggactccac catcatccct 650  
 tctatccat acagcatccc cagtataaat tctgtgatct gcattccatc 700  
 ctgtctcact gagaagtcca attccagtct atcaacatgt tacctaggat 750  
 acctcatcaa gaatcaaaga cttcttttaa tttctctttg atacaccott 800  
 gacaattttt catgaaatta ttctctctcc tgttcaataa atgattaccc 850  
 ttgcaactaa 860

<210> 256  
 <211> 180  
 <212> PRT  
 <213> Homo sapiens

<400> 256  
 Met Lys Met Leu Leu Leu Cys Leu Gly Leu Thr Leu Val Cys  
 1 5 10 15  
 Val His Ala Glu Glu Ala Ser Ser Thr Gly Arg Asn Phe Asn Val  
 20 25 30  
 Glu Lys Ile Asn Gly Glu Trp His Thr Ile Ile Leu Ala Ser Asp  
 35 40 45  
 Lys Arg Glu Lys Ile Glu Glu His Gly Asn Phe Arg Leu Phe Leu  
 50 55 60  
 Glu Gln Ile His Val Leu Glu Asn Ser Leu Val Leu Lys Val His  
 65 70 75  
 Thr Val Arg Asp Glu Glu Cys Ser Glu Leu Ser Met Val Ala Asp  
 80 85 90  
 Lys Thr Glu Lys Ala Gly Glu Tyr Ser Val Thr Tyr Asp Gly Phe  
 95 100 105  
 Asn Thr Phe Thr Ile Pro Lys Thr Asp Tyr Asp Asn Phe Leu Met  
 110 115 120

Ala His Leu Ile Asn Glu Lys Asp Gly Glu Thr Phe Gln Leu Met  
 125 130 135  
 Gly Leu Tyr Gly Arg Glu Pro Asp Leu Ser Ser Asp Ile Lys Glu  
 140 145 150  
 Arg Phe Ala Gln Leu Cys Glu Glu His Gly Ile Leu Arg Glu Asn  
 155 160 165  
 Ile Ile Asp Leu Ser Asn Ala Asn Arg Cys Leu Gln Ala Arg Glu  
 170 175 180

<210> 257  
 <211> 766  
 <212> DNA  
 <213> Homo sapiens

<400> 257  
 ggctcgagcg tttctgagcc aggggtgacc atgacctgct gcgaaggatg 50  
 gacatcctgc aatggattca gcctgctggt tctactgctg ttaggagtag 100  
 ttctcaatgc gatacctcta attgtcagct tagttgagga agaccaattt 150  
 tctcaaaacc ccactctctg ctttgagtgg tggttcccag gaattatagg 200  
 agcaggctcg atggccattc cagcaacaac aatgtccttg acagcaagaa 250  
 aaagagcgtg ctgcaacaac agaactggaa tgtttctttc atcatttttc 300  
 agtgtgatca cagtcattgg tgctctgtat tgcagtctga tatccatcca 350  
 ggctctctta aaaggtcctc tcatgtgtaa ttctccaagc aacagtaatg 400  
 ccaattgtga attttcattg aaaaacatca gtgacattca tccagaatcc 450  
 ttcaacttgc agtgggtttt caatgactct tgtgcacctc ctactgggtt 500  
 caataaacc accagtaacg acaccatggc gagtggctgg agagcatcta 550  
 gtttccactt cgattctgaa gaaaaacaac ataggcttat ccacttctca 600  
 gtatttttag gtctattgct tgttggaatt ctggaggtcc tgtttgggct 650  
 cagtcagata gtcacoggtt tccttggtctg tctgtgtgga gtctctaagc 700  
 gaagaagtca aattgtgtag ttaaatggga ataaaatgta agtatcagta 750  
 gtttgaaaaa aaaaaa 766

<210> 258  
 <211> 229  
 <212> PRT  
 <213> Homo sapiens

<400> 258  
 Met Thr Cys Cys Glu Gly Trp Thr Ser Cys Asn Gly Phe Ser Leu  
 1 5 10  
 Leu Val Leu Leu Leu Leu Gly Val Val Leu Asn Ala Ile Pro Leu  
 20 25 30  
 Ile Val Ser Leu Val Glu Glu Asp Gln Phe Ser Gln Asn Pro Ile



	35	40	45
Ser Cys Phe Glu Trp	Trp Phe Pro Gly	Ile Ile Gly Ala Gly	Leu
50	55	60	
Met Ala Ile Pro Ala	Thr Thr Met Ser	Leu Thr Ala Arg Lys	Arg
65	70	75	
Ala Cys Cys Asn Asn	Arg Thr Gly Met	Phe Leu Ser Ser Phe	Phe
80	85	90	
Ser Val Ile Thr Val	Ile Gly Ala Leu	Tyr Cys Met Leu Ile	Ser
95	100	105	
Ile Gln Ala Leu Leu	Lys Gly Pro Leu	Met Cys Asn Ser Pro	Ser
110	115	120	
Asn Ser Asn Ala Asn	Cys Glu Phe Ser	Leu Lys Asn Ile Ser	Asp
125	130	135	
Ile His Pro Glu Ser	Phe Asn Leu Gln	Trp Phe Phe Asn Asp	Ser
140	145	150	
Cys Ala Pro Pro Thr	Gly Phe Asn Lys	Pro Thr Ser Asn Asp	Thr
155	160	165	
Met Ala Ser Gly Trp	Arg Ala Ser Ser	Phe His Phe Asp Ser	Glu
170	175	180	
Glu Asn Lys His Arg	Leu Ile His Phe	Ser Val Phe Leu Gly	Leu
185	190	195	
Leu Leu Val Gly Ile	Leu Glu Val Leu	Phe Gly Leu Ser Gln	Ile
200	205	210	
Val Ile Gly Phe Leu	Gly Cys Leu Cys	Gly Val Ser Lys Arg	Arg
215	220	225	
Ser Gln Ile Val			

<210> 259  
 <211> 434  
 <212> DNA  
 <213> Homo sapiens

<400> 259  
 gtcgaatcca aatcactcat tgtgaaagct gagctcacag ccgaataagc 50  
 caccatgagg ctgtcagtgt gtctcctgat ggtctcgctg gccctttgct 100  
 gctaccaggc ccattgctctt gtctgccagc ctgttgcttc tgagatcaca 150  
 gtcttcttat totttaagtga cgtcgcggtta aacctccaag ttgccaaact 200  
 taatccacct ccagaagctc ttgcagccaa gttggaagtg aagcactgca 250  
 ccgatcagat atctttttaag aaacgactct cattgaaaaa gtcctggtgg 300  
 aaatagttaa aaaatgtggt gtgtgacatg taaaaatgct caacctggtt 350  
 tccaaagtct ttcaacgaca ccctgatctt cactaaaaat tgtaaagggt 400

tcaacacggtt gctttaataa atcacttgcc ctgc 434

<210> 260  
<211> 83  
<212> PRT  
<213> Homo sapiens

<400> 260  
Met Arg Leu Ser Val Cys Leu Leu Met Val Ser Leu Ala Leu Cys  
1 5 10 15  
Cys Tyr Gln Ala His Ala Leu Val Cys Pro Ala Val Ala Ser Glu  
20 25 30  
Ile Thr Val Phe Leu Phe Leu Ser Asp Ala Ala Val Asn Leu Gln  
35 40 45  
Val Ala Lys Leu Asn Pro Pro Pro Glu Ala Leu Ala Ala Lys Leu  
50 55 60  
Glu Val Lys His Cys Thr Asp Gln Ile Ser Phe Lys Lys Arg Leu  
65 70 75  
Ser Leu Lys Lys Ser Trp Trp Lys  
80

<210> 261  
<211> 636  
<212> DNA  
<213> Homo sapiens

<400> 261  
atccgtttctc tgcgctgcca gctcagggtga gccctcgcca aggtgacctc 50  
gcaggacact ggtgaaggag cagtgaggaa cctgcagagt cacacagttg 100  
ctgaccaatt gagctgtgag cctggagcag atccgtgggc tgcagacccc 150  
cgccccagtg cctctcccc tgcagccctg cccctegaac tgtgacatgg 200  
agagagtgac cctggccctt ctctactgg caggcctgac tgccttggaa 250  
gccaatgacc catttgccaa taaagacgat cccttctact atgactggaa 300  
aaacctgcag ctgagcggac tgatctgcgg agggctcctg gccattgctg 350  
ggatcgcggc agttctgagt ggcaaatgca aatacaagag cagccagaag 400  
cagcacagtc ctgtacctga gaaggccatc ccaatcatca ctccaggctc 450  
tgccactact tgotgagcac aggaactggcc tccagggatg gactgaagcc 500  
taacactggc cccagcacc tctccccctg ggaggcotta tctcaagga 550  
aggacttctc tccaagggca ggctgttagg cccctttctg atcaggaggc 600  
ttctttatga attaaactcg cccaccacc cctca 636

<210> 262  
<211> 89  
<212> PRT  
<213> Homo sapiens

<400> 262  
Met Glu Arg Val Thr Leu Ala Leu Leu Leu Leu Ala Gly Leu Thr  
1 5 10 15  
Ala Leu Glu Ala Asn Asp Pro Phe Ala Asn Lys Asp Asp Pro Phe  
20 25 30  
Tyr Tyr Asp Trp Lys Asn Leu Gln Leu Ser Gly Leu Ile Cys Gly  
35 40 45  
Gly Leu Leu Ala Ile Ala Gly Ile Ala Ala Val Leu Ser Gly Lys  
50 55 60  
Cys Lys Tyr Lys Ser Ser Gln Lys Gln His Ser Pro Val Pro Glu  
65 70 75  
Lys Ala Ile Pro Leu Ile Thr Pro Gly Ser Ala Thr Thr Cys  
80 85

<210> 263  
<211> 1676  
<212> DNA  
<213> Homo sapiens

<400> 263  
ggagaagagg ttgtgtggga caagctgctc cgcacagaag gatgtcgctg 50  
ctgagcctgc cctggctggg cctcagaccg gtggcaatgt ccccatggct 100  
actcctgctg ctggttgtgg gctcctggct actgccgcg atcctggctt 150  
ggacctatgc cttctataac aactgccgcc ggctccagt tttccacag 200  
ccccaaaac ggaactggtt ttgggggtcac ctgggcctga tcaactctac 250  
agaggagggc ttgaaggact cgacccagat gtggccacc tattccagg 300  
gctttacggt atgggtgggt cccatcatcc ccttcatcgt tttatgccac 350  
cctgacacca tccggtctat caccaatgcc tcagctgcca ttgcaccaa 400  
ggataatctc ttcacaggt tctgaagcc ctggctggga gaagggatac 450  
tgctgagtgg cggtgacaag tggagccgcc accgtcggat gctgacgccc 500  
gccttcatt tcaacatcct gaagtctat ataacgatct tcaacaagag 550  
tgcaaacatc atgcttgaca agtggcagca cctggcctca gagggcagca 600  
gtcgtctgga catgtttgag cacatcagcc tcatgacctt ggacagtcta 650  
cagaaatgca tcttcagctt tgacagccat tgtcaggaga ggcccagtga 700  
atatattgcc accatcttgg agctcagtc ccttgtagag aaaagaagcc 750  
agcatatcct ccagcacatg gactttctgt attacctctc ccatgacggg 800  
cggcgcttcc acagggcctg ccgcctgggt catgacttca cagacgtgt 850  
catccgggag cggcgtcgca cctcccccac tcagggtatt gatgattttt 900  
tcaaaagacaa agccaagtcc aagactttgg atttcattga tgtgcttctg 950

ctgagcaagg atgaagatgg gaaggcattg tcagatgagg atataagagc 1000  
 agaggctgac accttcattgt ttggaggcca tgacaccacg gccagtggcc 1050  
 tctcctgggt cctgtacaac cttgcgaggc acccagaata ccaggagcgc 1100  
 tgccgacagg aggtgcaaga gcttctgaag gaccgcgac ctaagagat 1150  
 tgaatgggac gacctggccc agctgccctt cctgacctg tgcgtgaagg 1200  
 agagcctgag gttacatccc ccagctccct tcatctccc atgctgcacc 1250  
 caggacattg ttctcccaga tggccgagtc atcccaaaag gcattacctg 1300  
 cctcatogat attatagggg tccatcacia cccaactgtg tggooggatc 1350  
 ctgaggtgta cgacccttc cgctttgacc cagagaacag caagggggagg 1400  
 tcacctctgg cttttattcc ttctctcgca gggcccagga actgcatcgg 1450  
 gcaggcgctc gccatggcgg agatgaaagt ggtcctggcg ttgatgctgc 1500  
 tgcacttcgg gttcctgcca gaccacactg agccccgcag gaagctggaa 1550  
 ttgatcatcg gcgccgagg cgggctttgg ctgcgggtgg agccctgaa 1600  
 tgtagccttg cagtgacttt ctgacctc caccgtttt ttgcagatt 1650  
 gtcacgaata aaacggtgct gtcaaa 1676

<210> 264  
 <211> 524  
 <212> PRT  
 <213> Homo sapiens

<400> 264  
 Met Ser Leu Leu Ser Leu Pro Trp Leu Gly Leu Arg Pro Val Ala  
 1 5 10 15  
 Met Ser Pro Trp Leu Leu Leu Leu Val Val Gly Ser Trp Leu  
 20 25 30  
 Leu Ala Arg Ile Leu Ala Trp Thr Tyr Ala Phe Tyr Asn Asn Cys  
 35 40 45  
 Arg Arg Leu Gln Cys Phe Pro Gln Pro Pro Lys Arg Asn Trp Phe  
 50 55 60  
 Trp Gly His Leu Gly Leu Ile Thr Pro Thr Glu Glu Gly Leu Lys  
 65 70 75  
 Asp Ser Thr Gln Met Ser Ala Thr Tyr Ser Gln Gly Phe Thr Val  
 80 85 90  
 Trp Leu Gly Pro Ile Ile Pro Phe Ile Val Leu Cys His Pro Asp  
 95 100 105  
 Thr Ile Arg Ser Ile Thr Asn Ala Ser Ala Ala Ile Ala Pro Lys  
 110 115 120  
 Asp Asn Leu Phe Ile Arg Phe Leu Lys Pro Trp Leu Gly Glu Gly  
 125 130 135

Ile	Leu	Leu	Ser	Gly	Gly	Asp	Lys	Trp	Ser	Arg	His	Arg	Arg	Met
				140					145					150
Leu	Thr	Pro	Ala	Phe	His	Phe	Asn	Ile	Leu	Lys	Ser	Tyr	Ile	Thr
				155					160					165
Ile	Phe	Asn	Lys	Ser	Ala	Asn	Ile	Met	Leu	Asp	Lys	Trp	Gln	His
				170					175					180
Leu	Ala	Ser	Glu	Gly	Ser	Ser	Arg	Leu	Asp	Met	Phe	Glu	His	Ile
				185					190					195
Ser	Leu	Met	Thr	Leu	Asp	Ser	Leu	Gln	Lys	Cys	Ile	Phe	Ser	Phe
				200					205					210
Asp	Ser	His	Cys	Gln	Glu	Arg	Pro	Ser	Glu	Tyr	Ile	Ala	Thr	Ile
				215					220					225
Leu	Glu	Leu	Ser	Ala	Leu	Val	Glu	Lys	Arg	Ser	Gln	His	Ile	Leu
				230					235					240
Gln	His	Met	Asp	Phe	Leu	Tyr	Tyr	Leu	Ser	His	Asp	Gly	Arg	Arg
				245					250					255
Phe	His	Arg	Ala	Cys	Arg	Leu	Val	His	Asp	Phe	Thr	Asp	Ala	Val
				260					265					270
Ile	Arg	Glu	Arg	Arg	Arg	Thr	Leu	Pro	Thr	Gln	Gly	Ile	Asp	Asp
				275					280					285
Phe	Phe	Lys	Asp	Lys	Ala	Lys	Ser	Lys	Thr	Leu	Asp	Phe	Ile	Asp
				290					295					300
Val	Leu	Leu	Leu	Ser	Lys	Asp	Glu	Asp	Gly	Lys	Ala	Leu	Ser	Asp
				305					310					315
Glu	Asp	Ile	Arg	Ala	Glu	Ala	Asp	Thr	Phe	Met	Phe	Gly	Gly	His
				320					325					330
Asp	Thr	Thr	Ala	Ser	Gly	Leu	Ser	Trp	Val	Leu	Tyr	Asn	Leu	Ala
				335					340					345
Arg	His	Pro	Glu	Tyr	Gln	Glu	Arg	Cys	Arg	Gln	Glu	Val	Gln	Glu
				350					355					360
Leu	Leu	Lys	Asp	Arg	Asp	Pro	Lys	Glu	Ile	Glu	Trp	Asp	Asp	Leu
				365					370					375
Ala	Gln	Leu	Pro	Phe	Leu	Thr	Met	Cys	Val	Lys	Glu	Ser	Leu	Arg
				380					385					390
Leu	His	Pro	Pro	Ala	Pro	Phe	Ile	Ser	Arg	Cys	Cys	Thr	Gln	Asp
				395					400					405
Ile	Val	Leu	Pro	Asp	Gly	Arg	Val	Ile	Pro	Lys	Gly	Ile	Thr	Cys
				410					415					420
Leu	Ile	Asp	Ile	Ile	Gly	Val	His	His	Asn	Pro	Thr	Val	Trp	Pro
				425					430					435
Asp	Pro	Glu	Val	Tyr	Asp	Pro	Phe	Arg	Phe	Asp	Pro	Glu	Asn	Ser
				440					445					450

Lys Gly Arg Ser Pro Leu Ala Phe Ile Pro Phe Ser Ala Gly Pro  
 455 460 465  
 Arg Asn Cys Ile Gly Gln Ala Phe Ala Met Ala Glu Met Lys Val  
 470 475 480  
 Val Leu Ala Leu Met Leu Leu His Phe Arg Phe Leu Pro Asp His  
 485 490 495  
 Thr Glu Pro Arg Arg Lys Leu Glu Leu Ile Met Arg Ala Glu Gly  
 500 505 510  
 Gly Leu Trp Leu Arg Val Glu Pro Leu Asn Val Gly Leu Gln  
 515 520

<210> 265  
 <211> 584  
 <212> DNA  
 <213> Homo sapiens

<400> 265  
 caacagaagc caagaaggaa gccgtctatc ttgtggcgat catgtataag 50  
 ctggcctcct gctgtttgct ttccacagga ttcttaaact ctctcttctc 100  
 tcttctctct cttgactcca gggaaatata ctttcaactc tcagcacctc 150  
 atgaagacgc gcgcttaact ccggaggagc tagaagagc ttcccttcta 200  
 cagatattgc cagagatgct ggggtgcagaa agaggggata ttctcaggaa 250  
 agcagactca agtaccaaca tttttaaccc aagaggaaat ttgagaaagt 300  
 ttcaggattt ctctggacaa gatcctaaca ttttactgag tcattctttg 350  
 gccagaatct ggaaaccata caagaaacgt gagactcctg attgctttctg 400  
 gaaataactgt gtctgaagtg aaataagcat ctgttagtca gctcagaaac 450  
 acccatctta gaatatgaaa aataacacaa tgcttgattt gaaaacagtg 500  
 tggagaaaaa ctaggcaaac tacaccctgt tcattgttac ctggaaaata 550  
 aatcctctat gttttgcaca aaaaaaaaaa aaaa 584

<210> 266  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<400> 266  
 Met Tyr Lys Leu Ala Ser Cys Cys Leu Leu Phe Thr Gly Phe Leu  
 1 5 10 15  
 Asn Pro Leu Leu Ser Leu Pro Leu Leu Asp Ser Arg Glu Ile Ser  
 20 25 30  
 Phe Gln Leu Ser Ala Pro His Glu Asp Ala Arg Leu Thr Pro Glu  
 35 40 45  
 Glu Leu Glu Arg Ala Ser Leu Leu Gln Ile Leu Pro Glu Met Leu  
 50 55 60

Gly Ala Glu Arg Gly Asp Ile Leu Arg Lys Ala Asp Ser Ser Thr  
65 70  
Asn Ile Phe Asn Pro Arg Gly Asn Leu Arg Lys Phe Gln Asp Phe  
80 85 90  
Ser Gly Gln Asp Pro Asn Ile Leu Leu Ser His Leu Leu Ala Arg  
95 100 105  
Ile Trp Lys Pro Tyr Lys Lys Arg Glu Thr Pro Asp Cys Phe Trp  
110 115 120  
Lys Tyr Cys Val

<210> 267  
<211> 654  
<212> DNA  
<213> Homo sapiens

<400> 267  
gaacattttt agttcccaag gaatgtacat cagccccacg gaagctaggc 50  
cacctctggg atgggggttg tggtttaaaa caaacgccag tcatacctata 100  
taaggacctg acagccacca ggcaccacct ccgccaggaa ctgcaggccc 150  
acctgtctgc aaccocagctg aggccatgcc ctcccaggg accgtctgca 200  
gcctcctgct ccteggcagc ctctggctgg acttggccat ggcaggctcc 250  
agcttctcta gccctgaaca ccagagagtc cagcagagaa aggagtcgaa 300  
gaagccacca gccaaagctgc agccccgagc tctagcaggc tggctccgcc 350  
cggaagatgg aggtcaagca gaaggggcag aggatgaact ggaagtcagg 400  
ttcaacgccc cctttgatgt tggaatcaag ctgtcagggg ttcagtacca 450  
gcagcacagc caggccctgg ggaagtttct tcaggacatc ctctgggaag 500  
aggccaaga ggccccagcc gacaagtgtat cggccacaag ccttactcac 550  
ctctctctaa gtttagaagc gctcatctgg cttttcgctt gcttctgcag 600  
caactcccac gactgttgta caagctcagg aggcgaataa atgttcaaac 650  
tgta 654

<210> 268  
<211> 117  
<212> PRT  
<213> Homo sapiens

<400> 268  
Met Pro Ser Pro Gly Thr Val Cys Ser Leu Leu Leu Gly Met  
1 5 10 15  
Leu Trp Leu Asp Leu Ala Met Ala Gly Ser Ser Phe Leu Ser Pro  
20 25 30  
Glu His Gln Arg Val Gln Gln Arg Lys Glu Ser Lys Lys Pro Pro  
35 40 45

Ala	Lys	Leu	Gln	Pro	Arg	Ala	Leu	Ala	Gly	Trp	Leu	Arg	Pro	Glu
				50					55					60
Asp	Gly	Gly	Gln	Ala	Glu	Gly	Ala	Glu	Asp	Glu	Leu	Glu	Val	Arg
				65					70					75
Phe	Asn	Ala	Pro	Phe	Asp	Val	Gly	Ile	Lys	Leu	Ser	Gly	Val	Gln
				80					85					90
Tyr	Gln	Gln	His	Ser	Gln	Ala	Leu	Gly	Lys	Phe	Leu	Gln	Asp	Ile
				95					100					105
Leu	Trp	Glu	Glu	Ala	Lys	Glu	Ala	Pro	Ala	Asp	Lys			
				110					115					

<210> 269  
 <211> 1332  
 <212> DNA  
 <213> Homo sapiens

<400> 269  
 cggccacagc tggcatgctc tgccctgatcg ccactcctgct gtatgtcctc 50  
 gtccagtagc tcgtgaaccc cggggtgctc cgcacggacc ccagatgtca 100  
 agaatatgaa cactgtggctg ctgttctctc cctgttctcc ggtgcagggtg 150  
 cagaccctga tagtcgtgat catcgggatg ctctgtctcc tctgtggactt 200  
 tcttggtctg gtgcacactgg gccagctgct catcttccac atctacatga 250  
 gtatgtctcc caccctaagc ccccgatccc cccaaggctg ggtggctcaga 300  
 gctgctcact ttacacctct acttgagtat gtccctaacc ctgagccccc 350  
 cagcctctgg gccagagtct ttgtcccccg tgtgcgcatg tgttcagggt 400  
 cagcctctcc cagaagtgg atcatggaca aaaagggcaa atcacaggaa 450  
 gaaattaaat ccatgaggac ccagcaggcc cagcaagaag ctgaactcac 500  
 gccgagacct gcaggagtgg tgccagggtc ttgaagtaac aagtttaaaa 550  
 tgttcagaga caatggaatg gaattctatta ggcaagaaca ggacattatg 600  
 aaataaggac aggtggactt ccaaaaacac aagtagaat tctaacaatg 650  
 aaatatatta caggcagggt acccactaac caaacaactg aagcgagagc 700  
 tgtgtgtctg cttggtctca cagtgggcac agcggtaggc ggtcagtcac 750  
 gttgtcgaac gacggagggt aaactcccca gccccaagaa aacctgtgtt 800  
 ggaagtaaca acaacctccc tgcctctggc accagccgtt ttggtcatgg 850  
 tgggccagct gcaaacgctc ttccattctc tgggcagtag tggccccgag 900  
 gctgtggcct ctccaggggt ttctgtggac acgggcagca gagtgtgtcc 950  
 agggccagcc ccaagaatgc cctgtctctg acagcttgcc caaccctgg 1000  
 tcagggcaga gggagtggg tgggtcaggc tctgggctca cctccatctc 1050



cagagcatcc cctgcctgca gttgtggcaa gaacgcccag ctcagaatga 1100  
 acacacccca ccaagagcct ccttgttcat aaccacaggt tacacctaaa 1150  
 accactgtcc ccacacaacc ctgggggatgt tttaaaacac acacctctaa 1200  
 cgcatacttt acagtcactg ttgtcttgcc tgagggttga atttttttta 1250  
 atgaaagtgc aatgaaaatc actggattaa atcctacgga cacagagctg 1300  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1332

<210> 270  
 <211> 142  
 <212> PRT  
 <213> Homo sapiens

<400> 270  
 Met Asn Thr Trp Leu Leu Phe Leu Pro Leu Phe Pro Val Gln Val  
 1 5 10 15  
 Gln Thr Leu Ile Val Val Ile Ile Gly Met Leu Val Leu Leu Leu  
 20 25 30  
 Asp Phe Leu Gly Leu Val His Leu Gly Gln Leu Leu Ile Phe His  
 35 40 45  
 Ile Tyr Leu Ser Met Ser Pro Thr Leu Ser Pro Arg Ser Pro Gln  
 50 55 60  
 Gly Trp Val Val Arg Ala Ala His Leu Thr Pro Leu Leu Glu Tyr  
 65 70 75  
 Val Pro Asn Pro Glu Pro Pro Thr Pro Gly Ala Arg Val Phe Val  
 80 85 90  
 Pro Arg Val Arg Met Cys Ser Gly Ser Ala Ser Pro Arg Ser  
 95 100 105  
 Ile Met Asp Lys Lys Gly Lys Ser Gln Glu Glu Ile Lys Ser Met  
 110 115 120  
 Arg Thr Gln Gln Ala Gln Gln Glu Ala Glu Leu Thr Pro Arg Pro  
 125 130 135  
 Ala Gly Val Val Pro Gly Ala  
 140

<210> 271  
 <211> 1484  
 <212> DNA  
 <213> Homo sapiens

<400> 271  
 ggagtgcaga tggcatcctt cggttcttcc agacaagctg caagacgctg 50  
 accatggcca agatggagct ctogaaggcc ttctctggcc agcggacact 100  
 cctatctgcc atcctcagca tgctatcact cagcttctcc acaacatccc 150  
 tgctcagcaa ctactggttt gtgggcacac agaaggtgcc caagcccctg 200  
 tgcgagaaag gtcgtgcagc caagtgtttt gacatgccag tgtccctgga 250

tggagatacc aacacatcca ccaggagggt ggtacaatac aactgggaga 300  
 ctggggatga ccggtttccc ttccggagct tccggagtgg catgtggcta 350  
 tcctgtgagg aaactgtgga agaaccaggg gagaggtgcc gaagtttcat 400  
 tgaacttaca ccaccagcca agagaggtga gaaaggacta ctggaatttg 450  
 ccacgttgca aggcccatgt cacccactc tccgatttgg agggaagcgg 500  
 ttgatggaga aggettccct cccctcccct cccctggggc tttgtggcaa 550  
 aaatcctatg gttatccctg ggaacgcaga tcacctatc cggacttcaa 600  
 ttcatcagct tctcctgct actaacagac ttgctactca ctgggaaccc 650  
 tgctgtggg ctcaaaactga gcgcctttgc tgctgtttcc tctgtcctgt 700  
 cagggttcct ggggatggg gccacatga tgtattcaca agtcttccaa 750  
 gcgactgtca acttgggtcc agaagactgg agaccacatg tttggaatta 800  
 tggctgggcc ttctacatgg cctggctctc cttcacctgc tgcattggct 850  
 cgctgtcac caccttcaac acgtacacca ggaagggtgt ggagtccaag 900  
 tgcaagcata gtaagagctt caaggaaaac ccgaactgcc taaccacatca 950  
 ccatcagtgt ttccctcggc ggctgtcaag tgcagccccc accgtgggtc 1000  
 ctttgaccag ctaccaccag tatcataatc agcccatcca ctctgtctct 1050  
 gagggagtcg acttctactc cgagctgcgg aacaagggat ttcaaaggag 1100  
 ggcoagccag gagctgaaag aagcagttag gtcattctgt gaggaagagc 1150  
 agtgtttaga gttaaagcggg ttgggggagt aggccttgagc cctaccttac 1200  
 acgtctgtg attatcaaca tgtgcttaag ccaacatccg tctcttgagc 1250  
 atgggtttta gaggtacga ataaggctat gaataagggt tatctttaag 1300  
 tctaaggga ttctgggtg ccaactgctc ctttctctc acagctccat 1350  
 cttgtttcac ccaccccaca tctcacacat ccagaattcc cttctttact 1400  
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 gtaaaatata cttcccgacc ttaaggatct gaaa 1484

<210> 272  
 <211> 285  
 <212> PRT  
 <213> Homo sapiens

<400> 272  
 Met Ala Lys Met Glu Leu Ser Lys Ala Phe Ser Gly Gln Arg Thr  
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 Leu Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser Phe Ser Thr  
 20 25 30  
 Thr Ser Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln Lys Val

	35	40	45
Pro Lys Pro Leu Cys Glu Lys Gly Leu Ala Lys Cys Phe Asp	50	55	60
Met Pro Val Ser Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu	65	70	75
Val Val Gln Tyr Asn Trp Glu Thr Gly Asp Asp Arg Phe Ser Phe	80	85	90
Arg Ser Phe Arg Ser Gly Met Trp Leu Ser Cys Glu Glu Thr Val	95	100	105
Glu Glu Pro Gly Glu Arg Cys Arg Ser Phe Ile Glu Leu Thr Pro	110	115	120
Pro Ala Lys Arg Gly Glu Lys Gly Leu Leu Glu Phe Ala Thr Leu	125	130	135
Gln Gly Pro Cys His Pro Thr Leu Arg Phe Gly Gly Lys Arg Leu	140	145	150
Met Glu Lys Ala Ser Leu Pro Ser Pro Pro Leu Gly Leu Cys Gly	155	160	165
Lys Asn Pro Met Val Ile Pro Gly Asn Ala Asp His Leu His Arg	170	175	180
Thr Ser Ile His Gln Leu Pro Pro Ala Thr Asn Arg Leu Ala Thr	185	190	195
His Trp Glu Pro Cys Leu Trp Ala Gln Thr Glu Arg Leu Cys Cys	200	205	210
Cys Phe Leu Cys Pro Val Arg Ser Pro Gly Asp Gly Gly Pro His	215	220	225
Asp Val Phe Thr Ser Leu Pro Ser Asp Cys Gln Leu Gly Ser Arg	230	235	240
Arg Leu Glu Thr Thr Cys Leu Glu Leu Trp Leu Gly Leu Leu His	245	250	255
Gly Leu Ala Leu Leu His Leu Leu His Gly Val Gly Cys His His	260	265	270
Leu Gln His Val His Gln Asp Gly Ala Gly Val Gln Val Gln Ala	275	280	285

<210> 273  
 <211> 1158  
 <212> DNA  
 <213> Homo sapiens

<400> 273  
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 ctcaacttaag tctcaggcct gtcagcagct cctgtggaca ttgccatccc 150  
 ctctggtagc cttcagagca aacaggacaa cctatgttat ggatgtttcc 200

accaaccagg gtagtggcat ggagcaccgt aaccatctgt gcttctgtga 250  
 tctctatgac agagccactt ctccacctct gaaatgttcc ctgctctgaa 300  
 atctggcatg agatggcaca ggtgaccacg cagaagccac cagaatcttg 350  
 cctgccttat tctctctccc aagtctgttc tcttattgtc aacctcaga 400  
 caacaggctg gcgccaatgg cattacagag aaagcaatct gtgtggctag 450  
 tgggcagatt accatgcaag cccagggaga aatggaggag cttttagacc 500  
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 aatggggcca tgtgaatgca gctgctctgt tctccctaacc ctgaggaaaa 800  
 accaaagga agcaacagga acttctgcaa ctgggttttta tcggaaagat 850  
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 cagctcccc gtagccatct ccagggtgac ggaaccaggt gtattacctg 1050  
 ctggaaccaa ggaactaac aatgtagggt actagtgaat accccaatgg 1100  
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 caactgaaa 1158

<210> 274  
 <211> 86  
 <212> PRT  
 <213> Homo sapiens

<400> 274  
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 20 25 30  
 Leu Leu Trp Thr Leu Pro Ser Pro Leu Val Ala Phe Arg Ala Asn  
 35 40 45  
 Arg Thr Thr Tyr Val Met Asp Val Ser Thr Asn Gln Gly Ser Gly  
 50 55 60  
 Met Glu His Arg Asn His Leu Cys Phe Cys Asp Leu Tyr Asp Arg  
 65 70 75  
 Ala Thr Ser Pro Pro Leu Lys Cys Ser Leu Leu  
 80 85

<210> 275  
 <211> 2694  
 <212> DNA  
 <213> Homo sapiens

<400> 275  
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 attagtttgt cctttggagg agcaatcgga ctgatgtttt tgatgcttgg 150  
 atgtgcctt ccaatataca acaataactg gccctctttt gttctatttt 200  
 tttacatctt ttcacctatt ccatactgca tagcaagaag attagtggat 250  
 gatacagatg ctatgagtaa cgcttgtaag gaacttgcca tttttcttac 300  
 aacgggcatt gtcgtgtcag cttttggact ccctattgta tttgccagag 350  
 cacatctgat tagtgggga gottgtgcac ttgtctcac aggaacaca 400  
 gtactctttg caactatact aggccttttc ttggctcttg gaagcaatga 450  
 cgacttcagc tggcagcagt ggtgaaaaga aattactgaa ctattgtcaa 500  
 atggaacttc tgtcatttgt tggccattca cgcacacagg agatggggca 550  
 gttaatgctg aatggtatag caagcctctt ggggggtatt tagtgctcc 600  
 cttctcactt ttattgtaag catactattt tcacagagac ttgctgaagg 650  
 attaaaagga ttttctctt tgaaaaagct tgactgattt cacacttatt 700  
 tatagtatgc tttttgttgt gtctgtctga atttaaatat ttatgtgttt 750  
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 ttttaatgta atcatttgca ttggttagga attcagaatt ccgcggctc 850  
 tattacttgt caagtacatc ttttctctta aaattattta gctccatta 900  
 ttacaaaaaa ttataaaaat aagttttcag tcagtcagga tgacatcact 950  
 cccaatgtta tgcagacata cagacgggtg gcatacgtta tagactgtat 1000  
 actcagtgca aatatagctg catttatacc tcagaggggc caagtgttaa 1050  
 tgcccatgcc ctccgttaag ggttggttgtt tttactggta gacagatgtt 1100  
 ttgtggattg aaaattattt tatggaattg ctacagagga gtgcttttct 1150  
 tctcaattgt tagaagaatt tatgttaaac tttaaggtaa ggggttaaaa 1200  
 acatttttga gataagggtt ttatttatgt ttattattgt tagagtga 1250  
 tgcaatgtgg gaagaaatga cattgaaatt ccagtttttg aatcctgttt 1300  
 ctattttataa gtgaaatttg tgatctocta tcaacctttc atgttttacc 1350  
 ctgttaaaat ggacatacat ggaaccacta ctgatgaggg acagttgtat 1400  
 gtttgcatca tatatgccag aaaaccttcc tctgcttctt ctttttgact 1450

tatttggtat gttgtatata ttacataaaa taacttttca aatatagttt 1500  
aataaacactt agaagtgttt acttacctgg aaaataattg ctatgcgcta 1550  
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cttgtagtc ttacagataa ttcattgcatt aacagtttaa gatttagacc 1650  
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gagttaatgc aaagtagcca agtccagcta tatagcagct tcagaaacat 1850  
acctgaccaa aaaattccca gtaaccaggc atgatcaatt tatagtggtc 1900  
gtttacatct aataattatc aggacttttt tcagaggtgg gttataaaaa 1950  
cattcaagtt ggtctgacag tattttgtta aggatatttt tttgtatgtt 2000  
tattcagtat acttacataa aaattatttc gccatcagcc aaaactcagt 2050  
aatcatgaca gctgtctgtt gttttatgaa gtttatttct caagaaaatg 2100  
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tgatgaaca ataaagattt taaatatcta ttttaaaaaa aaaa 2694

<210> 276

<211> 131

<212> PRT

<213> Homo sapiens

<400> 276

Met	Ala	Gly	Ile	Lys	Ala	Leu	Ile	Ser	Leu	Ser	Phe	Gly	Gly	Ala
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Ile	Gly	Leu	Met	Phe	Leu	Met	Leu	Gly	Cys	Ala	Leu	Pro	Ile	Tyr
			20					25					30	
Asn	Lys	Tyr	Trp	Pro	Leu	Phe	Val	Leu	Phe	Phe	Tyr	Ile	Leu	Ser

	35		40		45
Pro Ile Pro Tyr	Cys Ile Ala Arg Arg	Leu Val Asp Asp Thr	Asp		
	50	55	60		
Ala Met Ser Asn Ala	Cys Lys Glu Leu Ala	Ile Phe Leu Thr Thr			
	65	70	75		
Gly Ile Val Val Ser	Ala Phe Gly Leu Pro	Ile Val Phe Ala Arg			
	80	85	90		
Ala His Leu Ile Glu	Trp Gly Ala Cys Ala	Leu Val Leu Thr Gly			
	95	100	105		
Asn Thr Val Ile Phe	Ala Thr Ile Leu Gly Phe	Phe Leu Val Phe			
	110	115	120		
Gly Ser Asn Asp Asp	Phe Ser Trp Gln Gln Trp				
	125	130			

<210> 277  
 <211> 4104  
 <212> DNA  
 <213> Homo sapiens

<400> 277  
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 cgccgcgcgc cgacactccc caccgccgcg cgccgcgcgc ccgcgcgcgc 200  
 caaagcatga gtgagccgcg tctctgcagc tgccgggggc gcgaatggca 250  
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 ctggaaaagg atttctgacc gagcgcttcc aatggacatt ctccagtctc 700  
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 gtca 4104

<210> 278  
 <211> 522  
 <212> PRT  
 <213> Homo sapiens

<400> 278  
 Met Asp Phe Leu Leu Leu Gly Leu Cys Leu Tyr Trp Leu Leu Arg  
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 20 25 30  
 Met Leu Pro Ala Ala Pro Ser Gly Cys Pro Gln Leu Cys Arg Cys  
 35 40 45  
 Glu Gly Arg Leu Leu Tyr Cys Glu Ala Leu Asn Leu Thr Glu Ala  
 50 55 60  
 Pro His Asn Leu Ser Gly Leu Leu Gly Leu Ser Leu Arg Tyr Asn  
 65 70 75  
 Ser Leu Ser Glu Leu Arg Ala Gly Gln Phe Thr Gly Leu Met Gln  
 80 85 90  
 Leu Thr Trp Leu Tyr Leu Asp His Asn His Ile Cys Ser Val Gln  
 95 100 105  
 Gly Asp Ala Phe Gln Lys Leu Arg Arg Val Lys Glu Leu Thr Leu  
 110 115 120  
 Ser Ser Asn Gln Ile Thr Gln Leu Pro Asn Thr Thr Phe Arg Pro  
 125 130 135  
 Met Pro Asn Leu Arg Ser Val Asp Leu Ser Tyr Asn Lys Leu Gln  
 140 145 150  
 Ala Leu Ala Pro Asp Leu Phe His Gly Leu Arg Lys Leu Thr Thr  
 155 160 165  
 Leu His Met Arg Ala Asn Ala Ile Gln Phe Val Pro Val Arg Ile  
 170 175 180  
 Phe Gln Asp Cys Arg Ser Leu Lys Phe Leu Asp Ile Gly Tyr Asn  
 185 190 195  
 Gln Leu Lys Ser Leu Ala Arg Asn Ser Phe Ala Gly Leu Phe Lys  
 200 205 210  
 Leu Thr Glu Leu His Leu Glu His Asn Asp Leu Val Lys Val Asn  
 215 220 225  
 Phe Ala His Phe Pro Arg Leu Ile Ser Leu His Ser Leu Cys Leu  
 230 235 240  
 Arg Arg Asn Lys Val Ala Ile Val Val Ser Ser Leu Asp Trp Val  
 245 250 255  
 Trp Asn Leu Glu Lys Met Asp Leu Ser Gly Asn Glu Ile Glu Tyr  
 260 265 270  
 Met Glu Pro His Val Phe Glu Thr Val Pro His Leu Gln Ser Leu  
 275 280 285

Gln Leu Asp Ser Asn Arg Leu Thr Tyr Ile Glu Pro Arg Ile Leu  
 290 295 300  
 Asn Ser Trp Lys Ser Leu Thr Ser Ile Thr Leu Ala Gly Asn Leu  
 305 310 315  
 Trp Asp Cys Gly Arg Asn Val Cys Ala Leu Ala Ser Trp Leu Ser  
 320 325 330  
 Asn Phe Gln Gly Arg Tyr Asp Gly Asn Leu Gln Cys Ala Ser Pro  
 335 340 345  
 Glu Tyr Ala Gln Gly Glu Asp Val Leu Asp Ala Val Tyr Ala Phe  
 350 355 360  
 His Leu Cys Glu Asp Gly Ala Glu Pro Thr Ser Gly His Leu Leu  
 365 370 375  
 Ser Ala Val Thr Asn Arg Ser Asp Leu Gly Pro Pro Ala Ser Ser  
 380 385 390  
 Ala Thr Thr Leu Ala Asp Gly Gly Glu Gly Gln His Asp Gly Thr  
 395 400 405  
 Phe Glu Pro Ala Thr Val Ala Leu Pro Gly Gly Glu His Ala Glu  
 410 415 420  
 Asn Ala Val Gln Ile His Lys Val Val Thr Gly Thr Met Ala Leu  
 425 430 435  
 Ile Phe Ser Phe Leu Ile Val Val Leu Val Leu Tyr Val Ser Trp  
 440 445 450  
 Lys Cys Phe Pro Ala Ser Leu Arg Gln Leu Arg Gln Cys Phe Val  
 455 460 465  
 Thr Gln Arg Arg Lys Gln Lys Gln Lys Gln Thr Met His Gln Met  
 470 475 480  
 Ala Ala Met Ser Ala Gln Glu Tyr Tyr Val Asp Tyr Lys Pro Asn  
 485 490 495  
 His Ile Glu Gly Ala Leu Val Ile Ile Asn Glu Tyr Gly Ser Cys  
 500 505 510  
 Thr Cys His Gln Gln Pro Ala Arg Glu Cys Glu Val  
 515 520

<210> 279

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 279

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<210> 280

<211> 709

<212> DNA

<213> Homo sapiens

<400> 280  
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 caccgacttc gacgtcgag ccaactggag ccagaaccgg acccgtgag 150  
 ccggcggcgc cgttgagttc ccggcggaca agatggtgtc agtcctggtg 200  
 caagaaggtc acgccgtctc agacatgctc ctgccgtgg atggggaaact 250  
 cgtcctggct tcaggagccg gattcggcgt ctcagacgtg ggctcgacc 300  
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 cttcttgtg gacgcgagc gcgtgccctg ccgccacgac gacgtcttct 450  
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 ggacctggct gttttcctgg cgtcccgccg gggccgcta cgttccacg 600  
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 tgcgtctgcg gcaacgcgga ggcgagccg tggatctgag cggccctgct 700  
 ccagcccct 709

<210> 281  
 <211> 229  
 <212> PRT  
 <213> Homo sapiens

<400> 281  
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 Leu Thr Gln Ala Val Ser Lys Leu Trp Val Pro Asn Thr Asp Phe  
 20 25 30  
 Asp Val Ala Ala Asn Trp Ser Gln Asn Arg Thr Pro Cys Ala Gly  
 35 40 45  
 Gly Ala Val Glu Phe Pro Ala Asp Lys Met Val Ser Val Leu Val  
 50 55 60  
 Gln Glu Gly His Ala Val Ser Asp Met Leu Leu Pro Leu Asp Gly  
 65 70 75  
 Glu Leu Val Leu Ala Ser Gly Ala Gly Phe Gly Val Ser Asp Val  
 80 85 90  
 Gly Ser His Leu Asp Cys Gly Ala Gly Glu Pro Ala Val Phe Arg  
 95 100 105  
 Asp Ser Asp Arg Phe Ser Trp His Asp Pro His Leu Trp Arg Ser  
 110 115 120  
 Gly Asp Glu Ala Pro Gly Leu Phe Phe Val Asp Ala Glu Arg Val  
 125 130 135

Pro Cys Arg His Asp Asp Val Phe Phe Pro Pro Ser Ala Ser Phe  
140 145 150

Arg Val Gly Leu Gly Pro Gly Ala Ser Pro Val Arg Val Arg Ser  
155 160 165

Ile Ser Ala Leu Gly Arg Thr Phe Thr Arg Asp Glu Asp Leu Ala  
170 175 180

Val Phe Leu Ala Ser Arg Ala Gly Arg Leu Arg Phe His Gly Pro  
185 190 195

Gly Ala Leu Ser Val Gly Pro Glu Asp Cys Ala Asp Pro Ser Gly  
200 205 210

Cys Val Cys Gly Asn Ala Glu Ala Gln Pro Trp Ile Cys Ala Ala  
215 220 225

Leu Leu Gln Pro

<210> 282  
<211> 644  
<212> DNA  
<213> Homo sapiens

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cctcatgtac ctgtttcctc tctggatgtt gtccactgaa attccatga 550  
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<211> 77  
<212> PRT  
<213> Homo sapiens

<400> 283  
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Cys Ser Ala Phe	Trp Trp His Asn Lys	Gly Leu Ala Leu Ile Phe			
	35	40			
Cys Ile Leu Gln Ser Leu Ala Leu Thr	Trp Tyr Ser Leu Ser Phe				
	50	55			
Ile Pro Phe Ala Arg Asp Ala Val Lys	Lys Cys Phe Ala Val Cys				
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Leu Ala					

<210> 284  
 <211> 2623  
 <212> DNA  
 <213> Homo sapiens

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<211> 477  
 <212> PRT  
 <213> Homo sapiens

<400> 285

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Leu Leu Val Ser Phe	Asp Gly Phe Arg Trp	Asp Tyr Leu Tyr Lys
35	40	45
Val Pro Thr Pro His	Phe His Tyr Ile Met	Lys Tyr Gly Val His
50	55	60
Val Lys Gln Val Thr	Asn Val Phe Ile Thr	Lys Thr Tyr Pro Asn
65	70	75
His Tyr Thr Leu Val	Thr Gly Leu Phe Ala	Glu Asn His Gly Ile
80	85	90
Val Ala Asn Asp Met	Phe Asp Pro Ile Arg	Asn Lys Ser Phe Ser
95	100	105
Leu Asp His Met Asn	Ile Tyr Asp Ser Lys	Phe Trp Glu Glu Ala
110	115	120
Thr Pro Ile Trp Ile	Thr Asn Gln Arg Ala	Gly His Thr Ser Gly
125	130	135
Ala Ala Met Trp Pro	Gly Thr Asp Val Lys	Ile His Lys Arg Phe
140	145	150
Pro Thr His Tyr Met	Pro Tyr Asn Glu Ser	Val Ser Phe Glu Asp
155	160	165
Arg Val Ala Lys Ile	Val Glu Trp Phe Thr	Ser Lys Glu Pro Ile
170	175	180
Asn Leu Gly Leu Leu	Tyr Trp Glu Asp Pro	Asp Asp Met Gly His
185	190	195
His Leu Gly Pro Asp	Ser Pro Leu Met Gly	Pro Val Ile Ser Asp
200	205	210
Ile Asp Lys Lys Leu	Gly Tyr Leu Ile Gln	Met Leu Lys Lys Ala
215	220	225
Lys Leu Trp Asn Thr	Leu Asn Leu Ile Ile	Thr Ser Asp His Gly
230	235	240
Met Thr Gln Cys Ser	Glu Glu Arg Leu Ile	Glu Leu Asp Gln Tyr
245	250	255
Leu Asp Lys Asp His	Tyr Thr Leu Ile Asp	Gln Ser Pro Val Ala
260	265	270
Ala Ile Leu Pro Lys	Glu Gly Lys Phe Asp	Glu Val Tyr Glu Ala
275	280	285
Leu Thr His Ala His	Pro Asn Leu Thr Val	Tyr Lys Lys Glu Asp



290	295	300
Val Pro Glu Arg Trp His Tyr Lys Tyr	Asn Ser Arg Ile Gln Pro	
305	310	315
Ile Ile Ala Val Ala Asp Glu Gly Trp His	Ile Leu Gln Asn Lys	
320	325	330
Ser Asp Asp Phe Leu Leu Gly Asn His Gly	Tyr Asp Asn Ala Leu	
335	340	345
Ala Asp Met His Pro Ile Phe Leu Ala His	Gly Pro Ala Phe Arg	
350	355	360
Lys Asn Phe Ser Lys Glu Ala Met Asn Ser	Thr Asp Leu Tyr Pro	
365	370	375
Leu Leu Cys His Leu Leu Asn Ile Thr Ala	Met Pro His Asn Gly	
380	385	390
Ser Phe Trp Asn Val Gln Asp Leu Leu Asn	Ser Ala Met Pro Arg	
395	400	405
Val Val Pro Tyr Thr Gln Ser Thr Ile Leu	Leu Pro Gly Ser Val	
410	415	420
Lys Pro Ala Glu Tyr Asp Gln Glu Gly Ser	Tyr Pro Tyr Phe Ile	
425	430	435
Gly Val Ser Leu Gly Ser Ile Ile Val Ile	Val Phe Phe Val Ile	
440	445	450
Phe Ile Lys His Leu Ile His Ser Gln Ile	Pro Ala Leu Gln Asp	
455	460	465
Met His Ala Glu Ile Ala Gln Pro Leu Leu	Gln Ala	
470	475	

<210> 286

<211> 1337

<212> DNA

<213> Homo sapiens

<400> 286

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<210> 287  
 <211> 255  
 <212> PRT  
 <213> Homo sapiens

<400> 287  
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 Val Gly Asp Asp Tyr His Ala Trp Asn Ile Asn Tyr Lys Lys Trp  
 35 40 45  
 Glu Asn Glu Glu Glu Glu Glu Glu Glu Gln Pro Pro Pro Thr  
 50 55 60  
 Pro Val Ser Gly Glu Glu Gly Arg Ala Ala Pro Asp Val Ala  
 65 70 75  
 Pro Ala Pro Gly Pro Ala Pro Arg Ala Pro Leu Asp Phe Arg Gly  
 80 85 90  
 Met Leu Arg Lys Leu Phe Ser Ser His Arg Phe Gln Val Ile Ile  
 95 100 105  
 Ile Cys Leu Val Val Leu Asp Ala Leu Leu Val Leu Ala Glu Leu  
 110 115 120

Ile	Leu	Asp	Leu	Lys	Ile	Ile	Gln	Pro	Asp	Lys	Asn	Asn	Tyr	Ala
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Ala	Met	Val	Phe	His	Tyr	Met	Ser	Ile	Thr	Ile	Leu	Val	Phe	Phe
				140					145					150
Met	Met	Glu	Ile	Ile	Phe	Lys	Leu	Phe	Val	Phe	Arg	Leu	Ser	Ser
				155					160					165
Phe	Thr	Thr	Ser	Leu	Arg	Ser	Trp	Met	Pro	Val	Val	Val	Val	Val
				170					175					180
Ser	Phe	Ile	Leu	Asp	Ile	Val	Leu	Leu	Phe	Gln	Glu	His	Gln	Phe
				185					190					195
Glu	Ala	Leu	Gly	Leu	Leu	Ile	Leu	Leu	Arg	Leu	Trp	Arg	Val	Ala
				200					205					210
Arg	Ile	Ile	Asn	Gly	Ile	Ile	Ile	Ser	Val	Lys	Thr	Arg	Ser	Glu
				215					220					225
Arg	Gln	Leu	Leu	Arg	Leu	Lys	Gln	Met	Asn	Val	Gln	Leu	Ala	Ala
				230					235					240
Lys	Ile	Gln	His	Leu	Glu	Phe	Ser	Cys	Ser	Glu	Lys	Pro	Leu	Asp
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<210> 288

<211> 3334

<212> DNA

<213> Homo sapiens

<400> 288

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 <211> 469  
 <212> PRT  
 <213> Homo sapiens

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 Lys Ser Ile Phe Lys Leu Ser Val Phe Ile Pro Ser Gln Glu Phe  
 35 40 45  
 Ser Thr Tyr Arg Gln Trp Lys Gln Lys Ile Val Gln Ala Gly Asp  
 50 55 60  
 Lys Asp Leu Asp Gly Gln Leu Asp Phe Glu Glu Phe Val His Tyr  
 65 70 75  
 Leu Gln Asp His Glu Lys Lys Leu Arg Leu Val Phe Lys Ile Leu  
 80 85 90

Asp	Lys	Lys	Asn	Asp	Gly	Arg	Ile	Asp	Ala	Gln	Glu	Ile	Met	Gln	95	100	105
Ser	Leu	Arg	Asp	Leu	Gly	Val	Lys	Ile	Ser	Glu	Gln	Gln	Ala	Glu	110	115	120
Lys	Ile	Leu	Lys	Ser	Met	Asp	Lys	Asn	Gly	Thr	Met	Thr	Ile	Asp	125	130	135
Trp	Asn	Glu	Trp	Arg	Asp	Tyr	His	Leu	Leu	His	Pro	Val	Glu	Asn	140	145	150
Ile	Pro	Glu	Ile	Ile	Leu	Tyr	Trp	Lys	His	Ser	Thr	Ile	Phe	Asp	155	160	165
Val	Gly	Glu	Asn	Leu	Thr	Val	Pro	Asp	Glu	Phe	Thr	Val	Glu	Glu	170	175	180
Arg	Gln	Thr	Gly	Met	Trp	Trp	Arg	His	Leu	Val	Ala	Gly	Gly	Gly	185	190	195
Ala	Gly	Ala	Val	Ser	Arg	Thr	Cys	Thr	Ala	Pro	Leu	Asp	Arg	Leu	200	205	210
Lys	Val	Leu	Met	Gln	Val	His	Ala	Ser	Arg	Ser	Asn	Asn	Met	Gly	215	220	225
Ile	Val	Gly	Gly	Phe	Thr	Gln	Met	Ile	Arg	Glu	Gly	Gly	Ala	Arg	230	235	240
Ser	Leu	Trp	Arg	Gly	Asn	Gly	Ile	Asn	Val	Leu	Lys	Ile	Ala	Pro	245	250	255
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Val	Gly	Ser	Asp	Gln	Glu	Thr	Leu	Arg	Ile	His	Glu	Arg	Leu	Val	275	280	285
Ala	Gly	Ser	Leu	Ala	Gly	Ala	Ile	Ala	Gln	Ser	Ser	Ile	Tyr	Pro	290	295	300
Met	Glu	Val	Leu	Lys	Thr	Arg	Met	Ala	Leu	Arg	Lys	Thr	Gly	Gln	305	310	315
Tyr	Ser	Gly	Met	Leu	Asp	Cys	Ala	Arg	Arg	Ile	Leu	Ala	Arg	Glu	320	325	330
Gly	Val	Ala	Ala	Phe	Tyr	Lys	Gly	Tyr	Val	Pro	Asn	Met	Leu	Gly	335	340	345
Ile	Ile	Pro	Tyr	Ala	Gly	Ile	Asp	Leu	Ala	Val	Tyr	Glu	Thr	Leu	350	355	360
Lys	Asn	Ala	Trp	Leu	Gln	His	Tyr	Ala	Val	Asn	Ser	Ala	Asp	Pro	365	370	375
Gly	Val	Phe	Val	Leu	Leu	Ala	Cys	Gly	Thr	Met	Ser	Ser	Thr	Cys	380	385	390
Gly	Gln	Leu	Ala	Ser	Tyr	Pro	Leu	Ala	Leu	Val	Arg	Thr	Arg	Met	395	400	405

Gln Ala Gln Ala Ser Ile Glu Gly Ala Pro Glu Val Thr Met Ser  
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Ser Leu Phe Lys His Ile Leu Arg Thr Glu Gly Ala Phe Gly Leu  
 425 430 435

Tyr Arg Gly Leu Ala Pro Asn Phe Met Lys Val Ile Pro Ala Val  
 440 445 450

Ser Ile Ser Tyr Val Val Tyr Glu Asn Leu Lys Ile Thr Leu Gly  
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Val Gln Ser Arg

<210> 290  
 <211> 1658  
 <212> DNA  
 <213> Homo sapiens

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 actagacaag tgtgttaaga gtgataagta aaatgcacgt ggagacaagt 1200  
 gcatccccag atctcagga cctccccctg cctgtcacct ggggagtga 1250  
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 aattgactgc cacttcgcaa ctacggggcg gctgcatttt agtaatgggt 1450  
 caaatgattc actttttatg atgcttccaa aggtgccttg gcttctcttc 1500  
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 aaaaaaaa 1658

<210> 291  
 <211> 282  
 <212> PRT  
 <213> Homo sapiens

<400> 291  
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 Ile Ser Gly Arg His Ser Ile Thr Val Thr Val Ala Ser Ala  
 35 40 45  
 Gly Asn Ile Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro  
 50 55 60  
 Asp Ile Lys Leu Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly  
 65 70 75  
 Val Leu Gly Leu Val His Glu Phe Lys Glu Gly Lys Asp Glu Leu  
 80 85 90  
 Ser Glu Gln Asp Glu Met Phe Arg Gly Thr Ala Val Phe Ala  
 95 100 105  
 Asp Gln Val Ile Val Gly Asn Ala Ser Leu Arg Leu Lys Asn Val  
 110 115 120  
 Gln Leu Thr Asp Ala Gly Thr Tyr Lys Cys Tyr Ile Ile Thr Ser  
 125 130 135  
 Lys Gly Lys Gly Asn Ala Asn Leu Glu Tyr Lys Thr Gly Ala Phe  
 140 145 150  
 Ser Met Pro Glu Val Asn Val Asp Tyr Asn Ala Ser Ser Glu Thr



	155		160		165
Leu Arg Cys Glu	Ala Pro Arg Trp Phe	Pro Gln Pro Thr Val Val			
	170	175			180
Trp Ala Ser Gln	Val Asp Gln Gly Ala	Asn Phe Ser Glu Val Ser			
	185	190			195
Asn Thr Ser Phe	Glu Leu Asn Ser Glu	Asn Val Thr Met Lys Val			
	200	205			210
Val Ser Val Leu	Tyr Asn Val Thr Ile	Asn Asn Thr Tyr Ser Cys			
	215	220			225
Met Ile Glu Asn	Asp Ile Ala Lys Ala	Thr Gly Asp Ile Lys Val			
	230	235			240
Thr Glu Ser Glu	Ile Lys Arg Arg Ser	His Leu Gln Leu Leu Asn			
	245	250			255
Ser Lys Ala Ser	Leu Cys Val Ser Ser	Phe Phe Ala Ile Ser Trp			
	260	265			270
Ala Leu Leu Pro	Leu Ser Pro Tyr Leu	Met Leu Lys			
	275	280			

<210> 292  
 <211> 1484  
 <212> DNA  
 <213> Homo sapiens

<400> 292  
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 tgaagcgggc ctccgccggc ctgcagcggg ttcatgagcc gacctggggc 150  
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 aaaacgtaag ttgactact gcgagtgctg gacgcagctc tgtggatctc 400  
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 cctgtgggcc atcagagttc ctttccctg gacagtctgg agaagacag 550  
 aggtcggggt ttgggattga agaccagacc ccatctgagc ccttctcca 600  
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 aatttcaact tgcatacaaa gctcagtgag taagaccagc gggcaacagt 750  
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 aacctttctg cccacgcagc tctcttcctg ctaacatctc aggcctcccag 1050  
 cccagccacc attactgtgg cctgatctgg actatcatgg tggcaggttc 1100  
 catggactgc agaactccag ctgcatggaa agggccagct gcagactttg 1150  
 agccagaaat gcaaacggga ggcctctggg actcagtcag agcgcttttg 1200  
 ctgaatgagg ggtggaaccg aggggaagaag gtgcgtcgga gtggcagatg 1250  
 caggaataga gctgtctatt agccttgctt gccccaccca tgaggtaggc 1300  
 agaaatcctc actgccagcc cctcttaaac aggtagagag ctgtgagccc 1350  
 cagccccacc tgactccagc acacctggcg agtagtagct gtcaataaat 1400  
 ctatgtaaac agacaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1450  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1484

<210> 293  
 <211> 180  
 <212> PRT  
 <213> Homo sapiens

<400> 293  
 Met Ala Ala Ser Leu Gly Gln Val Leu Ala Leu Val Leu Val Ala  
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 Gly Leu Gln Arg Val His Glu Pro Thr Trp Ala Gln Gln Leu Leu  
 35 40 45  
 Gln Glu Met Lys Thr Leu Phe Leu Asn Thr Glu Tyr Leu Met Pro  
 50 55 60  
 Phe Leu Leu Asn Gln Cys Gly Ser Leu Leu Tyr Tyr Leu Thr Leu  
 65 70 75  
 Ala Ser Thr Asp Leu Thr Leu Ala Val Pro Ile Cys Asn Ser Leu  
 80 85 90  
 Ala Ile Ile Phe Thr Leu Ile Val Gly Lys Ala Leu Gly Glu Asp  
 95 100 105  
 Ile Gly Gly Lys Arg Lys Leu Asp Tyr Cys Glu Cys Gly Thr Gln  
 110 115 120  
 Leu Cys Gly Ser Arg His Thr Cys Val Ser Ser Phe Pro Glu Pro  
 125 130 135  
 Ile Ser Pro Glu Trp Val Arg Thr Arg Pro Phe Pro Ile Leu Pro  
 140 145 150

Phe Pro Leu Gln Leu Phe Cys Phe Leu Val Ala Ile Arg Val Pro  
155 160 165

Phe Pro Trp Thr Val Trp Arg Lys Thr Glu Ala Gly Val Trp Asp  
170 175 180

<210> 294

<211> 1164

<212> DNA

<213> Homo sapiens

<400> 294

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tcgaaaagat tccgcaataa aactttgccg gtgggaagta cctagtga 150
cggcctaaga tgccacttct tctcatgtcc caggcttgag gccctgtggt 200
ccccatcctt gggagaagtc agctccagca ccatgaaggg catcctcggt 250
gctgggtatca ctgcagtgct tgttgagct gtagaatctc tgaagtgcgt 300
gcagtgtaat tcattgggaaa aatcctgtgt caacagcatt gcctctgaat 350
gtccctcaca tgccaacacc agctgtatca gctcctcagc cagctcctct 400
ctagagacac cagtcagatt ataccagaat atgttctgct cagcggagaa 450
ctgcagtgag gagacacaca ttacagcctt cactgtccac gtgtctgctg 500
aagaacactt tcattttgta agccagtgct gccaaagaaa ggaatgcagc 550
aacaccagcg atgccctgga ccctcccctg aagaacgtgt ccagcaacgc 600
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cctggaaatg ctatgaagaa gaacagtggt tctttctagt tgcagaactt 700
aagaatgaca ttgagtctaa gagtctctgt ctgaaaggct gttccaacgt 750
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gagtcattct tcgaaagttt gagtgtgcaa atgtaaacag cttaaccccc 850
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ttgttcttca ttattaaagc actggttcat tcactgccaa aaaaaaaaaa 1150
aaaaaaaaaa aaaa 1164
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<210> 295

<211> 237

<212> PRT

<213> Homo sapiens

<400> 295

Met Lys Gly Ile Leu Val Ala Gly Ile Thr Ala Val Leu Val Ala  
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Ala Val Glu Ser Leu Ser Cys Val Gln Cys Asn Ser Trp Glu Lys  
20 25 30

Ser Cys Val Asn Ser Ile Ala Ser Glu Cys Pro Ser His Ala Asn  
35 40 45

Thr Ser Cys Ile Ser Ser Ser Ala Ser Ser Ser Leu Glu Thr Pro  
50 55 60

Val Arg Leu Tyr Gln Asn Met Phe Cys Ser Ala Glu Asn Cys Ser  
65 70 75

Glu Glu Thr His Ile Thr Ala Phe Thr Val His Val Ser Ala Glu  
80 85 90

Glu His Phe His Phe Val Ser Gln Cys Cys Gln Gly Lys Glu Cys  
95 100 105

Ser Asn Thr Ser Asp Ala Leu Asp Pro Pro Leu Lys Asn Val Ser  
110 115 120

Ser Asn Ala Glu Cys Pro Ala Cys Tyr Glu Ser Asn Gly Thr Ser  
125 130 135

Cys Arg Gly Lys Pro Trp Lys Cys Tyr Glu Glu Glu Gln Cys Val  
140 145 150

Phe Leu Val Ala Glu Leu Lys Asn Asp Ile Glu Ser Lys Ser Leu  
155 160 165

Val Leu Lys Gly Cys Ser Asn Val Ser Asn Ala Thr Cys Gln Phe  
170 175 180

Leu Ser Gly Glu Asn Lys Thr Leu Gly Gly Val Ile Phe Arg Lys  
185 190 195

Phe Glu Cys Ala Asn Val Asn Ser Leu Thr Pro Thr Ser Ala Pro  
200 205 210

Thr Thr Ser His Asn Val Gly Ser Lys Ala Ser Leu Tyr Leu Leu  
215 220 225

Ala Leu Ala Ser Leu Leu Leu Arg Gly Leu Leu Pro  
230 235

<210> 296

<211> 1245

<212> DNA

<213> Homo sapiens

<400> 296

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ccagcccat ggtcccgcc gccggcgccg tgctgtgggt cctgctgctg 150

aatctgggtc cccgggcggc gggggcccaa ggcctgaccc agactccgac 200  
cgaaatgcag cgggtcagtt tacgctttgg gggcccatg acccgagct 250  
accggagcac cgcccgact ggtcttcccc ggaagacaag gataatccta 300  
gaggacgaga atgatgccat ggccgacgcc gaccgcctgg ctggaccagc 350  
ggctgcccag ctcttggccg ccacgggtgc caccggcttt agccggtcgt 400  
ccgcattaa cgaggaggat gggctctcag aagagggggg tgtgattaat 450  
gccggaagg atagcaccag cagagagctt cccagtgcga ctcccatac 500  
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cccgagccgg tggccgtcac cctcaccac agccatgcca tctcctgagg 700  
atctgcggct ggtgctgatg ccttggggcc cgtggcactg ccaactgcaag 750  
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gcgccttoga gttggggcgc tgagccagct ccgcacggag cacaagcctt 850  
gcacctatca acaatgtccc tgcaaccgac ttcggaaga gtgcccctg 900  
gacacaagtc tctgtactga caccaactgt gcctctcaga gcaccaccag 950  
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ccagcctgcc accgcgcagc cctgcccag cctggcttt ttgaaacgg 1050  
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agagatgcaa ccaatagaca gaaaccagag gtaatggcca ctccatccac 1150  
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ccactagata tttttagtac agaaaaacaa aactggaaaa caca 1245

<210> 297  
<211> 341  
<212> FRT  
<213> Homo sapiens

<400> 297  
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Leu Gly Pro Arg Ala Ala Gly Ala Gln Gly Leu Thr Gln Thr Pro  
20 25 30  
Thr Glu Met Gln Arg Val Ser Leu Arg Phe Gly Gly Pro Met Thr  
35 40 45  
Arg Ser Tyr Arg Ser Thr Ala Arg Thr Gly Leu Pro Arg Lys Thr  
50 55 60  
Arg Ile Ile Leu Glu Asp Glu Asn Asp Ala Met Ala Asp Ala Asp

	65	70	75
Arg Leu Ala Gly	Pro Ala Ala Ala Glu	Leu Leu Ala Ala Thr	Val
	80	85	90
Ser Thr Gly Phe	Ser Arg Ser Ser Ala	Ile Asn Glu Glu Asp	Gly
	95	100	105
Ser Ser Glu Glu	Gly Val Val Ile Asn	Ala Gly Lys Asp Ser	Thr
	110	115	120
Ser Arg Glu Leu	Pro Ser Ala Thr Pro	Asn Thr Ala Gly Ser	Ser
	125	130	135
Ser Thr Arg Phe	Ile Ala Asn Ser Gln	Glu Pro Glu Ile Arg	Leu
	140	145	150
Thr Ser Ser Leu	Pro Arg Ser Pro Gly	Arg Ser Thr Glu Asp	Leu
	155	160	165
Pro Gly Ser Gln	Ala Thr Leu Ser Gln	Trp Ser Thr Pro Gly	Ser
	170	175	180
Thr Pro Ser Arg	Trp Pro Ser Pro Ser	Pro Thr Ala Met Pro	Ser
	185	190	195
Pro Glu Asp Leu	Arg Leu Val Leu Met	Pro Trp Gly Pro Trp	His
	200	205	210
Cys His Cys Lys	Ser Gly Thr Met Ser	Arg Ser Arg Ser Gly	Lys
	215	220	225
Leu His Gly Leu	Ser Gly Arg Leu Arg	Val Gly Ala Leu Ser	Gln
	230	235	240
Leu Arg Thr Glu	His Lys Pro Cys Thr	Tyr Gln Gln Cys Pro	Cys
	245	250	255
Asn Arg Leu Arg	Glu Glu Cys Pro Leu	Asp Thr Ser Leu Cys	Thr
	260	265	270
Asp Thr Asn Cys	Ala Ser Gln Ser Thr	Thr Ser Thr Arg Thr	Thr
	275	280	285
Thr Thr Pro Phe	Pro Thr Ile His Leu	Arg Ser Ser Pro Ser	Leu
	290	295	300
Pro Pro Ala Ser	Pro Cys Pro Ala Leu	Ala Phe Trp Lys Arg	Val
	305	310	315
Arg Ile Gly Leu	Glu Asp Ile Trp Asn	Ser Leu Ser Ser Val	Phe
	320	325	330
Thr Glu Met Gln	Pro Ile Asp Arg Asn	Gln Arg	
	335	340	

<210> 298  
 <211> 2692  
 <212> DNA  
 <213> Homo sapiens

<400> 298  
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 gtgggtcacc gttgggtctt acctccagga aggtcacaaa gtgcctcagt 300  
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 tgcgcgtgct ggtgggcatg tgagatgagt gactgccggt gaattgtgtc 1900  
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 gcttaataaa tcaattccaa gcctcaaaaa aaaaaaaaaa aa 2692

<210> 299  
 <211> 320  
 <212> PRT  
 <213> Homo sapiens

<400> 299  
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 20 25 30  
 Asp Cys Val Leu Gln Cys Glu Glu Gln Asn Cys Ser Gly Gly Ala  
 35 40 45  
 Leu Asn His Phe Arg Ser Arg Gln Pro Ile Tyr Met Ser Leu Ala  
 50 55 60  
 Gly Trp Thr Cys Arg Asp Asp Cys Lys Tyr Glu Cys Met Trp Val  
 65 70 75



Thr Val Gly Leu Tyr Leu Gln Glu Gly His Lys Val Pro Gln Phe  
 80 85 90  
 His Gly Lys Trp Pro Phe Ser Arg Phe Leu Phe Phe Gln Glu Pro  
 95 100 105  
 Ala Ser Ala Val Ala Ser Phe Leu Asn Gly Leu Ala Ser Leu Val  
 110 115 120  
 Met Leu Cys Arg Tyr Arg Thr Phe Val Pro Ala Ser Ser Pro Met  
 125 130 135  
 Tyr His Thr Cys Val Ala Phe Ala Trp Val Ser Leu Asn Ala Trp  
 140 145 150  
 Phe Trp Ser Thr Val Phe His Thr Arg Asp Thr Asp Leu Thr Glu  
 155 160 165  
 Lys Met Asp Tyr Phe Cys Ala Ser Thr Val Ile Leu His Ser Ile  
 170 175 180  
 Tyr Leu Cys Cys Val Arg Thr Val Gly Leu Gln His Pro Ala Val  
 185 190 195  
 Val Ser Ala Phe Arg Ala Leu Leu Leu Leu Met Leu Thr Val His  
 200 205 210  
 Val Ser Tyr Leu Ser Leu Ile Arg Phe Asp Tyr Gly Tyr Asn Leu  
 215 220 225  
 Val Ala Asn Val Ala Ile Gly Leu Val Asn Val Val Trp Trp Leu  
 230 235 240  
 Ala Trp Cys Leu Trp Asn Gln Arg Arg Leu Pro His Val Arg Lys  
 245 250 255  
 Cys Val Val Val Val Leu Leu Leu Gln Gly Leu Ser Leu Leu Glu  
 260 265 270  
 Leu Leu Asp Phe Pro Pro Leu Phe Trp Val Leu Asp Ala His Ala  
 275 280 285  
 Ile Trp His Ile Ser Thr Ile Pro Val His Val Leu Phe Phe Ser  
 290 295 300  
 Phe Leu Glu Asp Asp Ser Leu Tyr Leu Leu Lys Glu Ser Glu Asp  
 305 310 315  
 Lys Phe Lys Leu Asp  
 320

<210> 300  
 <211> 1674  
 <212> DNA  
 <213> Homo sapiens

<400> 300  
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 gaaggtccgt gactatggct cccagagcc tgccttcac taggatggct 100  
 cctctgggca tgctgcttgg gctgctgatg gccgcctgct tcaccttctg 150



<211> 461  
 <212> PRT  
 <213> Homo sapiens

<400> 301

Met	Ala	Pro	Gln	Ser	Leu	Pro	Ser	Ser	Arg	Met	Ala	Pro	Leu	Gly	1	5	10	15
Met	Leu	Leu	Gly	Leu	Leu	Met	Ala	Ala	Cys	Phe	Thr	Phe	Cys	Leu	20	25	30	
Ser	His	Gln	Asn	Leu	Lys	Glu	Phe	Ala	Leu	Thr	Asn	Pro	Glu	Lys	35	40	45	
Ser	Ser	Thr	Lys	Glu	Thr	Glu	Arg	Lys	Glu	Thr	Lys	Ala	Glu	Glu	50	55	60	
Glu	Leu	Asp	Ala	Glu	Val	Leu	Glu	Val	Phe	His	Pro	Thr	His	Glu	65	70	75	
Trp	Gln	Ala	Leu	Gln	Pro	Gly	Gln	Ala	Val	Pro	Ala	Gly	Ser	His	80	85	90	
Val	Arg	Leu	Asn	Leu	Gln	Thr	Gly	Glu	Arg	Glu	Ala	Lys	Leu	Gln	95	100	105	
Tyr	Glu	Asp	Lys	Phe	Arg	Asn	Asn	Leu	Lys	Gly	Lys	Arg	Leu	Asp	110	115	120	
Ile	Asn	Thr	Asn	Thr	Tyr	Thr	Ser	Gln	Asp	Leu	Lys	Ser	Ala	Leu	125	130	135	
Ala	Lys	Phe	Lys	Glu	Gly	Ala	Glu	Met	Glu	Ser	Ser	Lys	Glu	Asp	140	145	150	
Lys	Ala	Arg	Gln	Ala	Glu	Val	Lys	Arg	Leu	Phe	Arg	Pro	Ile	Glu	155	160	165	
Glu	Leu	Lys	Lys	Asp	Phe	Asp	Glu	Leu	Asn	Val	Val	Ile	Glu	Thr	170	175	180	
Asp	Met	Gln	Ile	Met	Val	Arg	Leu	Ile	Asn	Lys	Phe	Asn	Ser	Ser	185	190	195	
Ser	Ser	Ser	Leu	Glu	Glu	Lys	Ile	Ala	Ala	Leu	Phe	Asp	Leu	Glu	200	205	210	
Tyr	Tyr	Val	His	Gln	Met	Asp	Asn	Ala	Gln	Asp	Leu	Leu	Ser	Phe	215	220	225	
Gly	Gly	Leu	Gln	Val	Val	Ile	Asn	Gly	Leu	Asn	Ser	Thr	Glu	Pro	230	235	240	
Leu	Val	Lys	Glu	Tyr	Ala	Ala	Phe	Val	Leu	Gly	Ala	Ala	Phe	Ser	245	250	255	
Ser	Asn	Pro	Lys	Val	Gln	Val	Glu	Ala	Ile	Glu	Gly	Gly	Ala	Leu	260	265	270	
Gln	Lys	Leu	Leu	Val	Ile	Leu	Ala	Thr	Glu	Gln	Pro	Leu	Thr	Ala	275	280	285	
Lys	Lys	Lys	Val	Leu	Phe	Ala	Leu	Cys	Ser	Leu	Leu	Arg	His	Phe				

290	295	300
Pro Tyr Ala Gln	Arg Gln Phe Leu Lys	Leu Gly Gly Leu Gln Val
305	310	315
Leu Arg Thr Leu	Val Gln Glu Lys Gly Thr	Glu Val Leu Ala Val
320	325	330
Arg Val Val Thr	Leu Leu Tyr Asp Leu	Val Thr Glu Lys Met Phe
335	340	345
Ala Glu Glu Glu	Ala Glu Leu Thr Gln	Glu Met Ser Pro Glu Lys
350	355	360
Leu Gln Gln Tyr	Arg Gln Val His Leu	Leu Pro Gly Leu Trp Glu
365	370	375
Gln Gly Trp Cys	Glu Ile Thr Ala His	Leu Leu Ala Leu Pro Glu
380	385	390
His Asp Ala Arg	Glu Lys Val Leu Gln	Thr Leu Gly Val Leu Leu
395	400	405
Thr Thr Cys Arg	Asp Arg Tyr Arg Gln	Asp Pro Gln Leu Gly Arg
410	415	420
Thr Leu Ala Ser	Leu Gln Ala Glu Tyr	Gln Val Leu Ala Ser Leu
425	430	435
Glu Leu Gln Asp	Gly Glu Asp Glu Gly	Tyr Phe Gln Glu Leu Leu
440	445	450
Gly Ser Val Asn	Ser Leu Leu Lys Glu	Leu Arg
455	460	

<210> 302  
 <211> 2136  
 <212> DNA  
 <213> Homo sapiens

<400> 302  
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 ccccccttc ccttccccg gggctctgggg gtgacattgc accgcgcccc 100  
 tcgtggggtc gcgttgccac cccacgcgga ctccccagct ggcgcgcccc 150  
 tcccatttgc ctgtcctggt caggccccca ccccccttcc cactcgacca 200  
 gccatggggg ctgcggtgtt ttccggctgc actttcgtcg cgttcggccc 250  
 ggccttcgcg cttttcttga tcaactgtgc tggggaccgc cttcgcgtta 300  
 tcactctggt cgcaggggca tttttctggc tgggtctcct gctcctggcc 350  
 tctgtggtct ggttcattct ggtccatgtg accgaccggt cagatgcccc 400  
 gctccagtac ggcctcctga tttttggtgc tgctgtctct gtcctctac 450  
 aggaggtgtt ccgctttgcc tactacaagc tgcttaagaa ggcagatgaa 500  
 gggtagcat cgctgagtga ggacggaaga tcacccatct ccatccgcca 550

gatggcctat gtttctggtc tctccttcgg tatcatcagt ggtgtcttct 600  
ctgttatcaa tattttggct gatgcacttg gccaggtgt ggttgggac 650  
catggagact caccctatta ctctctgact tcagccttcc tgacagcagc 700  
cattatcctg ctccatacct tttggggagt tgtgttcttt gatgcctgtg 750  
agaggagacg gtactgggtt ttgggccttg tggttgggag tcacctactg 800  
acatcgggac tgacattcct gaacccttg tatgaggcca gctgctgcc 850  
catctatgca gtcactgttt ccatggggct ctgggccttc atcacagctg 900  
gagggtccct cgaagtatt cagcgcagcc tcttgtgtaa ggactgacta 950  
cctggactga tcgcctgaca gatcccacct gctgtccac tgcccatgac 1000  
tgagcccagc ccagcccgg gtccattgcc cacattctct gtctccttct 1050  
cgtcgtgtcta cccactacc tccagggttt tgctttgtcc ttttgtgacc 1100  
gttagtctct aagctttacc aggagcagcc tgggttcagc cagtcaagtga 1150  
ctggtgggtt tgaatctgca cttatcccca ccacctggg accccttgt 1200  
tgtgtccagg actcccctg tgtcagtgtct ctgctctcac cctgcccaag 1250  
actcacctcc ctccctctct gcaggccgac ggaggaggga cagtgggtg 1300  
atggtgtatt ctgccctgag catcccaacc gaggactgag ggaacctagg 1350  
ggggacccct gggcctgggg tgccctcctg atgtcctgc cctgtatttc 1400  
tccatctcca gttctggaca gtgcagggtt ccaagaaaag ggacctagtt 1450  
tagccattgc cctggagatg aaattaatgg aggcctcaag atagatgagc 1500  
tctgagtttc tcagtactcc ctcaagactg gacatcttgg tcttttctc 1550  
aggcctgagg ggaaccatt tttggtgtga taaataccct aaactgcctt 1600  
ttttctttt ttgagtgagg gggaggagg aggtatatgt gaactcttct 1650  
aacctccttg ggctatattt tctctcctcg agttgtcctc catggctggg 1700  
ctcatttcgg tccctttctc ctgtgtccca gacctgggg gaaaggaagg 1750  
aagtgcattg ttgggaactg gcattactgg aactaatggt ttaacctcc 1800  
ttaaccacca gcacccctcc tctccccaag gtgaagtgga ggggtgtgtg 1850  
gtgagctgac cactccagag ctgcagtgcc actggaggag tcagactacc 1900  
atgacatcgt agggaaggag gggagatttt tttgtagttt ttaattgggg 1950  
tgtgggaggg gcggggaggt tttctataaa ctgtatcatt ttctgctgag 2000  
ggtggagtgt cccatccttt taatcaaggt gattgtgatt ttgactaata 2050  
aaaaagaatt tgtaaaaaaa aaaaaaaaaa aaaaaaaaaa 2100  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2136

<210> 303  
 <211> 247  
 <212> PRT  
 <213> Homo sapiens

<400> 303  
 Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe Gly  
 1 5 10 15  
 Pro Ala Phe Ala Leu Phe Leu Ile Thr Val Ala Gly Asp Pro Leu  
 20 25 30  
 Arg Val Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser  
 35 40 45  
 Leu Leu Leu Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr  
 50 55 60  
 Asp Arg Ser Asp Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly  
 65 70 75  
 Ala Ala Val Ser Val Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr  
 80 85 90  
 Tyr Lys Leu Leu Lys Lys Ala Asp Glu Gly Leu Ala Ser Leu Ser  
 95 100 105  
 Glu Asp Gly Arg Ser Pro Ile Ser Ile Arg Gln Met Ala Tyr Val  
 110 115 120  
 Ser Gly Leu Ser Phe Gly Ile Ile Ser Gly Val Phe Ser Val Ile  
 125 130 135  
 Asn Ile Leu Ala Asp Ala Leu Gly Pro Gly Val Val Gly Ile His  
 140 145 150  
 Gly Asp Ser Pro Tyr Tyr Phe Leu Thr Ser Ala Phe Leu Thr Ala  
 155 160 165  
 Ala Ile Ile Leu Leu His Thr Phe Trp Gly Val Val Phe Phe Asp  
 170 175 180  
 Ala Cys Glu Arg Arg Tyr Trp Ala Leu Gly Leu Val Val Gly  
 185 190 195  
 Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu Asn Pro Trp Tyr  
 200 205 210  
 Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val Ser Met Gly  
 215 220 225  
 Leu Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser Ile Gln  
 230 235 240  
 Arg Ser Leu Leu Cys Lys Asp  
 245

<210> 304  
 <211> 240  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> unsure  
<222> 108, 123, 126, 154, 198, 206, 217  
<223> unknown base

<400> 304  
aagctgggtt aaggaagcag aggaggggta gattcgttga gtgaggacgg 50  
aagatcaacc catttccatt ccgccagatg gcctatgttt ctggtctctc 100  
ccttcggnat catcagtggg gtnttntctg ttatcaatat ttggtgtgat 150  
gcanttgggc cagggtgtgg tgggatccat ggagactcac cctattantt 200  
cctganttca gctttntga cagcagccat tatcctgctc 240

<210> 305  
<211> 378  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 58, 94, 132, 186, 191, 220, 240, 248, 280, 311, 332  
<223> unknown base

<400> 305  
gaccgaccgt tcagatgcc ggttccagta cggcttcctg atttttgggtg 50  
ctgtgtntc tgtccttcta caggaggtgt tccgctttgc ctantacaag 100  
ctgcttaaga aggcagatga ggggttagca tngctgagtg aggacggaag 150  
atcaccatt tccatccgcc agatggccta tgttttgggt ntctccttcg 200  
gtatcatcag tgggtgtttt tctgttatca atattttggn tgatgcantt 250  
gggccagggt tggttgggat ccatggagan tcaccctatt aattcctgaa 300  
ttcagccttt ntgacagcag ccattatcct gntccatacc ttttggggag 350  
tttgtttttt tgatgcctgt gagaggag 378

<210> 306  
<211> 655  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1, 22, 129, 133, 184  
<223> unknown base

<400> 306  
ngttggagaa gtggcgcgga cnttcatttg gggtttcggt ttccccctt 50  
tccctttccc cggggtctgg ggtgacattg cacgggcccc tcgtgggggtc 100  
gcggtgccac cccacgcgga ctccccagnt gngcgccct tccattttgc 150  
ctgtcctggt caggccccca ccccccttc cacntgacca gccatggggg 200  
ctgcggtgtt ttcggtctgc actttctgctg cggtcgcccc ggccttcgctg 250

cttttcttga tcaactgtggc tggggaccgc cttcgcgtta tcaactcgtg 300  
 cgcaggggca tttttctggc tggctctcct gctcctggcc totgtggtct 350  
 ggttcactctt ggtccatgtg accgaccggt cagatgccgc gctccagtac 400  
 ggccctctga tttttggtgc tgctgtctct gtccctctac aggaggtgtt 450  
 ccgctttgcc tactacaagc tgcttaagaa ggcagatgag gggtagcat 500  
 cgctgagtga ggacggaaga tcacccatct ccacccgcca gatggcctat 550  
 gtttctggtc tctccttcgg tatcatcagt ggtgtcttct ctgttatcaa 600  
 tattttggct gatgcacttg ggccaggtgt ggttgggac catggagact 650  
 cacc 655

<210> 307  
 <211> 650  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 52, 89, 128  
 <223> unknown base

<400> 307  
 gtaaaagaaa gtggccggac cttcattggg gtttcgggtc cccctttcc 50  
 onttccccgg ggtctggggg tgacattgca ccgcgccnt cgtggggtcg 100  
 cgttgccacc ccacgaggac tcccagntg gcgcgccct ccattttgcc 150  
 tgcctgggtc agggcccccac ccccttccc acctgaccag ccattggggc 200  
 tgcggtgttt ttcgggctgc actttctgog cgttcggggc cggccttgc 250  
 gcttttcttg atcaactgtg ctggggaccg gcttcgcgtt atcatcctgg 300  
 tcgcaggggc atttttctgg ctggtctccc tgctcctggc ctctgtggtc 350  
 tggttcatct tggtcactgt gaccgaccgc tcagatgccg ggtccagta 400  
 cggcctcctg atttttgggt ctgctgtctc tgcctctcta caggaggtgt 450  
 tccgctttgc ctactacaag ctgcttaaga aggagatga ggggttagca 500  
 tcgctgagtg aggacggaag atcacccatc tccatccgc agatggccta 550  
 tgtttctggt ctctccttgc gtatcatcag tgggtctctc tctgttatca 600  
 atattttgac tgatgcactt ggccaggtg tgggtgggat ccattggagac 650

<210> 308  
 <211> 1570  
 <212> DNA  
 <213> Homo sapiens

<400> 308  
 gccccaggga gcagtggtg gttataactc agggccgggt cccagagccc 50



aggaggaagc	agtggtccagg	aaggcacagg	cctgagaagt	ctgcggctga	100
gctggggagca	aatccccacc	ccctacacct	ggggacaggg	caagtggagac	150
ctgggtgagg	tggctcagca	ggcagggaag	gagaggtgtc	tgtgcgtcct	200
gcaccacat	ctttctctgt	ccctcctctg	ccctgtctgg	aggctgctag	250
actcctatct	tctgaattct	atagtgcctg	ggtctcagcg	cagtgccgat	300
ggtggcccgct	ccttgtgggt	cctctctacc	tggggaaata	aggtgcagcg	350
gccatggcta	cagcaagacc	cccctggatg	tgggtgctct	gtgctctgat	400
cacagcccttg	cttctggggg	tcacagagca	tgttctcgcc	aacaatgatg	450
tttctgtga	ccaccctct	aacaccgtgc	cctctgggag	caaccaggac	500
ctgggagctg	gggcccggga	agacgcccgg	tcggatgaca	gcagcagccg	550
catcatcaat	ggatccgact	gcgatatgca	caccacgocg	tggcaggccg	600
cgtctgttct	aaggcccaac	cagctctact	gcggggcggt	gttgtgtcat	650
ccacagtggc	tgctcacggc	cgccactgc	aggaagaaa	tttccagagt	700
ccgtctcggc	cactactccc	tgctaccagt	ttatgaatct	gggcagcaga	750
tgttccaggg	ggtcaaatcc	atccccacc	ctggctactc	ccaccctggc	800
cactctaacg	acctcatgct	catcaaaactg	aacagaagaa	ttcgtccacc	850
taaagatgtc	agaccatcat	acgtctctct	tcattgtccc	tctgctggga	900
caaagtgctt	ggtgtctggc	tgggggacaa	ccaagagccc	ccaagtgcac	950
ttccctaagg	tctctcagtg	cttgaatatc	agcgtgctaa	gtcagaaaag	1000
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gtgacaaagc	aggtagagac	tctgtccagg	gtgattctgg	ggggcctgtg	1100
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tgccccggcc	aacagaccgg	gtgtctacac	gaacctctgc	aagttacca	1200
agtggatcca	ggaaaccatc	caggccaact	cctgagtcac	cccaggactc	1250
agcacaccgg	catccccacc	tgtctgacgg	acagccctga	cactccttcc	1300
agacctctat	tccttcccag	agatgtttag	aatgttcac	ttctccagccc	1350
ctgaccccat	gtctctctga	ctcagggtct	gcttccccca	cattgggctg	1400
accgtgtctc	tctagttgaa	ccctgggaac	aatttccaaa	actgtccagg	1450
gcggggggtg	cgtctcaatc	tccttggggc	acttctatcc	tcaagctcag	1500
ggcccatccc	ttctctgcag	ctctgaccca	aatttagtcc	cagaaataaa	1550
ctgaqaagtg	gaaaaaaaaa	1570			

<210> 309

<211> 293  
 <212> PRT  
 <213> Homo sapiens

<400> 309  
 Met Ala Thr Ala Arg Pro Pro Trp Met Trp Val Leu Cys Ala Leu  
 1 5 10 15  
 Ile Thr Ala Leu Leu Leu Gly Val Thr Glu His Val Leu Ala Asn  
 20 25 30  
 Asn Asp Val Ser Cys Asp His Pro Ser Asn Thr Val Pro Ser Gly  
 35 40 45  
 Ser Asn Gln Asp Leu Gly Ala Gly Ala Gly Glu Asp Ala Arg Ser  
 50 55 60  
 Asp Asp Ser Ser Ser Arg Ile Ile Asn Gly Ser Asp Cys Asp Met  
 65 70 75  
 His Thr Gln Pro Trp Gln Ala Ala Leu Leu Leu Arg Pro Asn Gln  
 80 85 90  
 Leu Tyr Cys Gly Ala Val Leu Val His Pro Gln Trp Leu Leu Thr  
 95 100 105  
 Ala Ala His Cys Arg Lys Lys Val Phe Arg Val Arg Leu Gly His  
 110 115 120  
 Tyr Ser Leu Ser Pro Val Tyr Glu Ser Gly Gln Gln Met Phe Gln  
 125 130 135  
 Gly Val Lys Ser Ile Pro His Pro Gly Tyr Ser His Pro Gly His  
 140 145 150  
 Ser Asn Asp Leu Met Leu Ile Lys Leu Asn Arg Arg Ile Arg Pro  
 155 160 165  
 Thr Lys Asp Val Arg Pro Ile Asn Val Ser His Cys Pro Ser  
 170 175 180  
 Ala Gly Thr Lys Cys Leu Val Ser Gly Trp Gly Thr Thr Lys Ser  
 185 190 195  
 Pro Gln Val His Phe Pro Lys Val Leu Gln Cys Leu Asn Ile Ser  
 200 205 210  
 Val Leu Ser Gln Lys Arg Cys Glu Asp Ala Tyr Pro Arg Gln Ile  
 215 220 225  
 Asp Asp Thr Met Phe Cys Ala Gly Asp Lys Ala Gly Arg Asp Ser  
 230 235 240  
 Cys Gln Gly Asp Ser Gly Gly Pro Val Val Cys Asn Gly Ser Leu  
 245 250 255  
 Gln Gly Leu Val Ser Trp Gly Asp Tyr Pro Cys Ala Arg Pro Asn  
 260 265 270  
 Arg Pro Gly Val Tyr Thr Asn Leu Cys Lys Phe Thr Lys Trp Ile  
 275 280 285  
 Gln Glu Thr Ile Gln Ala Asn Ser

<210> 310  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 310  
 tctctgagacc acccctctaa cacc 24

<210> 311  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 311  
 ctggaacatc tgctgcccag attc 24

<210> 312  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 312  
 gtcggatgac agcagcagcc gcatcatcaa tggatccgac tgcgatatgc 50

<210> 313  
 <211> 3010  
 <212> DNA  
 <213> Homo sapiens

<400> 313  
 atgggtcaacg accggtggaa gaccatgggc ggcgctgccc aacttgagga 50  
 ccggccgcgc gacaagccgc agcggccgag ctgcggctac gtgctgtgca 100  
 ccgtgtgtgt ggccttggtc gtgctgtgtg ctgtagctgt caccgggtgcc 150  
 gtgtctcttc tgaaccacgc ccacgcgcgc ggcacggcgc cccacctgt 200  
 cgtcagcact gggggtgccca gcgccaacag cgccctggtc actgtggaaa 250  
 gggcggagac ctgcgcacctc agcatcctca ttgaccgcgc ctgccccgac 300  
 ctccaccgaca gcttcgcacg cctggagagc gccacggcct cgggtgtgca 350  
 ggcgctgaca gagcaccagg ccagccacgc gctggtgggc gaccaggagc 400  
 aggagctgct ggacacgctg gccgaccagc tgccccggct gctggcccca 450  
 gcctcagagc tgcagacgga gtgcatgggg ctgcggaagg ggcattggcac 500  
 gctggggcag ggcctcagcg ccctgcagag tgagcagggc cgcctcatcc 550

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agcgacatcc	tggatgcct	gcagagggac	cgggggctgg	gccggccccg	650
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gctgtgccac	tggctcccg	ccccagact	gtctggacgt	cctcctaagc	750
ggacagcagg	acgatggcgt	ctactctgtc	tttccacccc	actaccggc	800
cggcttcacg	gtgtactgtg	acatgcgcac	ggacggcggc	ggctggacgg	850
tgtttcagcg	ccgggaggac	ggctccgtga	acttcttcgg	gggctgggac	900
gcgtaccgag	acggctttgg	caggctcacc	gggagcact	ggctagggct	950
caagaggatc	cacgcctga	ccacacaggc	tgctacagag	ctgcacgtgg	1000
acctggagg	ctttgagaat	ggcacggcct	atgcccgcta	cgggagcttc	1050
ggcgtgggct	tgttctccgt	ggacctgtag	gaagacgggt	accgcgtcac	1100
cgtggtgtac	tattccggca	ctgcaggcga	ctccctcctg	aagcacagcg	1150
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gagatgaaga	tccggccgggt	ccgggaggac	cgtagacgtg	gtgcaccttg	1400
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ttctgtgaat	gttctccacc	cacctgtgcc	tgcgggaccc	actctccagt	1500
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cacacatcgc	cttctgcgcg	tccccacccc	ctccatttgg	cagctcactg	1600
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tgcttgcccc	cactgtgact	ccggtgctgt	ttgcgctccc	ctggccagga	1700
tggtggagtc	tgccccaggc	accctctgcc	ctgccccggc	aaataccogg	1750
cattatgggg	acagagagca	gggggcagac	agcacccctg	gagtcctcct	1800
agcagatcgt	ggggaatgtc	aggtctctct	gaggtcaggt	ctgaggccag	1850
tatcctccag	ccctcccaat	gccaaacccc	accccgtttc	cctggtgccc	1900
agagaaccca	cctctccccc	aagggcctca	gcctggctgt	gggctgggtg	1950
gccccatcct	accaggccct	gaggtcagga	tggggagctg	ctgccttttg	2000
ggacccacgc	tccaaggctg	agaccagttc	cctggaggcc	acccaccctg	2050
tgccccgcga	ggcctggggt	ctgcagtcct	cttacctgct	tgccccacct	2100
gctctctgtc	tcaaataagg	cccaacccat	ccccaccaca	gctcccgccc	2150

gtcctcctac ctggggcagc cggggctgcc atcccatttc tctgcctct 2200  
 ggaagtggtg tggggccctg caccgtgggg ctggactgcg ctaatgggaa 2250  
 gctcttggtt ttctgggctg gggcctaggc agggctggga tgaggctgtg 2300  
 acaaccacca ccaccaattt cccagggact ccagggtcct gaggcctccc 2350  
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 ccggcccgcc gagtgggcaa gggacaggga ccacctcacc gggcaaatgg 2500  
 ggtcgggggg actggggcac cagaccaggc accacctgga cactttcttg 2550  
 ttgaatcctc ccaaacacca gcacgtgtc atccccactc cttgtgtgca 2600  
 cacatgcaga ggtgagaccc gcaggctccc aggaccagca gccacaaggg 2650  
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 ctctcctcgg gcaggagggg aggtggcttc ctccaaagga caccgatgg 2850  
 cagggtccta gggggtgtgg ggttcggttc tcccttcccc tcccaactga 2900  
 gtttgtgctt aaaaaacaat aaatttgact tggcaccact gggggttggt 2950  
 gggagaggcc gtgtgacctg gctctctgtc ccagtccac caggatcatc 3000  
 acatgcgcag 3010

<210> 314  
 <211> 461  
 <212> PRT  
 <213> Homo sapiens

<400> 314  
 Met Val Asn Asp Arg Trp Lys Thr Met Gly Gly Ala Ala Gln Leu  
 1 5 10  
 Glu Asp Arg Pro Arg Asp Lys Pro Gln Arg Pro Ser Cys Gly Tyr  
 20 25 30  
 Val Leu Cys Thr Val Leu Leu Ala Leu Ala Val Leu Leu Ala Val  
 35 40 45  
 Ala Val Thr Gly Ala Val Leu Phe Leu Asn His Ala His Ala Pro  
 50 55 60  
 Gly Thr Ala Pro Pro Pro Val Val Ser Thr Gly Ala Ala Ser Ala  
 65 70 75  
 Asn Ser Ala Leu Val Thr Val Glu Arg Ala Asp Ser Ser His Leu  
 80 85 90  
 Ser Ile Leu Ile Asp Pro Arg Cys Pro Asn Leu Thr Asp Ser Phe  
 95 100 105

Ala Arg Leu Glu	Ser Ala Gln Ala Ser	Val Leu Gln Ala Leu	Thr
110	110	115	120
Glu His Gln Ala	Gln Pro Arg Leu Val	Gly Asp Gln Glu Gln	Glu
125	125	130	135
Leu Leu Asp Thr	Leu Ala Asp Gln Leu	Pro Arg Leu Leu Ala	Arg
140	140	145	150
Ala Ser Glu Leu	Gln Thr Glu Cys Met	Gly Leu Arg Lys Gly	His
155	155	160	165
Gly Thr Leu Gly	Gln Gly Leu Ser Ala	Leu Gln Ser Glu Gln	Gly
170	170	175	180
Arg Leu Ile Gln	Leu Leu Ser Glu Ser	Gln Gly His Met Ala	His
185	185	190	195
Leu Val Asn Ser	Val Ser Asp Ile Leu	Asp Ala Leu Gln Arg	Asp
200	200	205	210
Arg Gly Leu Gly	Arg Pro Arg Asn Lys	Ala Asp Leu Gln Arg	Ala
215	215	220	225
Pro Ala Arg Gly	Thr Arg Pro Arg Gly	Cys Ala Thr Gly Ser	Arg
230	230	235	240
Pro Arg Asp Cys	Leu Asp Val Leu Leu	Ser Gly Gln Gln Asp	Asp
245	245	250	255
Gly Val Tyr Ser	Val Phe Pro Thr His	Tyr Pro Ala Gly Phe	Gln
260	260	265	270
Val Tyr Cys Asp	Met Arg Thr Asp Gly	Gly Gly Trp Thr Val	Phe
275	275	280	285
Gln Arg Arg Glu	Asp Gly Ser Val Asn	Phe Arg Gly Trp Asp	
290	290	295	300
Ala Tyr Arg Asp	Gly Phe Gly Arg Leu	Thr Gly Glu His Trp	Leu
305	305	310	315
Gly Leu Lys Arg	Ile His Ala Leu Thr	Thr Gln Ala Ala Tyr	Glu
320	320	325	330
Leu His Val Asp	Leu Glu Asp Phe Glu	Asn Gly Thr Ala Tyr	Ala
335	335	340	345
Arg Tyr Gly Ser	Phe Gly Val Gly Leu	Phe Ser Val Asp Pro	Glu
350	350	355	360
Glu Asp Gly Tyr	Pro Leu Thr Val Ala	Asp Tyr Ser Gly Thr	Ala
365	365	370	375
Gly Asp Ser Leu	Leu Lys His Ser Gly	Met Arg Phe Thr Thr	Lys
380	380	385	390
Asp Arg Asp Ser	Asp His Ser Glu Asn	Asn Cys Ala Ala Phe	Tyr
395	395	400	405
Arg Gly Ala Trp	Trp Tyr Arg Asn Cys	His Thr Ser Asn Leu	Asn
410	410	415	420

Gly Gln Tyr Leu Arg Gly Ala His Ala Ser Tyr Ala Asp Gly Val  
 425 430  
 Glu Trp Ser Ser Trp Thr Gly Trp Gln Tyr Ser Leu Lys Phe Ser  
 440 445 450  
 Glu Met Lys Ile Arg Pro Val Arg Glu Asp Arg  
 455 460

<210> 315  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 315  
 cacacgtcca acctcaatgg gcag 24

<210> 316  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 316  
 gaccagcagg gccaaaggaca agg 23

<210> 317  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 317  
 gttctctgag atgaagatcc ggccggtccg ggagtaccgc ttag 44

<210> 318  
 <211> 1841  
 <212> DNA  
 <213> Homo sapiens

<400> 318  
 gcagtcagag acttccctcg cccctcgctg ggaagaaca ttaggaatgc 50  
 cttttagtgc ctgtcttct gaactagctc acagtagccc ggcgccccc 100  
 ggcaatccga ccacatttca ctctcacgc ttaggaatc cagatgcagg 150  
 ccaagtacag cagcacgagg gacatgctgg atgatgatgg ggacaccacc 200  
 atgagcctgc attctcaagc ctctgccaca actcggcatc cagagcccc 250  
 gcgcacagag cacagggtc cctcttcaac gtggcgacca gtggccctga 300  
 cctgtgtgac ttgtgtcttg gtgtgtctga tagggctggc agccctgggg 350  
 cttttgtttt ttcagtacta ccagctctcc aatactggtc aagacaccat 400

ttctcaaagt gaagaaagat taggaaatac gtcccaagag ttgcaatctc 450  
 ttcaagtcca gaatataaag ctgtcaggaa gtctgcagca tgtggctgaa 500  
 aaactctgtc gtgagctgta taacaaagct ggagcacaca ggtgcagccc 550  
 ttgtacagaa caatggaaat ggcattggaga caattgctac cagttctata 600  
 aagacagcaa aagttgggag gactgtaaat atttctgocct tagtgaatac 650  
 tctaccatgc tgaagataaa caaacaagaa gacctggaat ttgccgcgtc 700  
 tcagagctac tctgagtttt tctactctta ttggacaggg cttttgcgcc 750  
 ctgacagtgg caaggcctgg ctgtggatgg atggaacccc tttcacttct 800  
 gaactgttcc atattataat agatgtcacc agcccaagaa gcagagactg 850  
 tgtggccatc ctcaatggga tgatcttctc aaaggactgc aaagaattga 900  
 agcgttgtgt ctgtgagaga agggcaggaa tggggaagcc agagagcctc 950  
 catgtccccc ctgaaacatt aggcgaaggt gactgattcg cctctctcaa 1000  
 ctacaaatag cagagtgcgc caggcgggtgc caagcaagg gctagttgag 1050  
 acattgggaa atggaacata atcaggaaag actatctctc tgactagtac 1100  
 aaaaagggtt ctctgttttc ctgttcagga tcaccagcat ttctgagctt 1150  
 ggggttatgc acgtatttaa cagtcacaag aagtcttatt tacatgccac 1200  
 caaccaacct cagaaaccca taatgtcatc tgccttcttg gcttagagat 1250  
 aacttttagc tctctttctt ctcaatgtct aatatcaacct cctgttttcc 1300  
 atgtcttctc tacaattggt ggaataagaa actttttgaa gttagaggaaa 1350  
 tacattgagg taacatcctt ttctctgaca gtcaagtagt ccatcagaaa 1400  
 ttggcagtc cttccagat tgtaccagca aatacacaag gaattctttt 1450  
 tgtttgttcc agttcatact agtcccttcc caatccatca gtaaagacct 1500  
 catctgcctt gtccatgccg ttcccaaca gggatgtcac ttgatatgag 1550  
 aatctcaaat ctcaatgcct tataagcatt ccttctctgt tccattaaga 1600  
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 gagagattaa agaccagaaa aaagtgagcc tcttcatctg cacctgtaat 1750  
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 actgaagatt taataataat aaatgtaaat actgtgaaaa a 1841

<210> 319  
 <211> 280  
 <212> PRT  
 <213> Homo sapiens



<400> 319

Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp Asp  
1 5 10 15

Gly Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr  
20 25 30

Arg His Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser  
35 40 45

Thr Trp Arg Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val  
50 55 60

Leu Leu Ile Gly Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr  
65 70 75

Tyr Gln Leu Ser Asn Thr Gly Gln Asp Thr Ile Ser Gln Met Glu  
80 85 90

Glu Arg Leu Gly Asn Thr Ser Gln Glu Leu Gln Ser Leu Gln Val  
95 100 105

Gln Asn Ile Lys Leu Ala Gly Ser Leu Gln His Val Ala Glu Lys  
110 115 120

Leu Cys Arg Glu Leu Tyr Asn Lys Ala Gly Ala His Arg Cys Ser  
125 130 135

Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln  
140 145 150

Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys  
155 160 165

Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp  
170 175 180

Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser  
185 190 195

Tyr Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu  
200 205 210

Trp Met Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile  
215 220 225

Ile Asp Val Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu  
230 235 240

Asn Gly Met Ile Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys  
245 250 255

Val Cys Glu Arg Arg Ala Gly Met Val Lys Pro Glu Ser Leu His  
260 265 270

Val Pro Pro Glu Thr Leu Gly Glu Gly Asp  
275 280

<210> 320

<211> 468

<212> DNA

<213> Homo sapiens

<220>  
<221> unsure  
<222> 59, 95, 149, 331, 364, 438, 446  
<223> unknown base

<400> 320  
aattttcacc gctgtaggaa tccagatgca ggccaagtac agcagcacga 50  
gggacatgnt ggatgatgat gggacaccac catgagcctg catnttcaag 100  
cttttgccac aattcggcat ccagagccccc ggcgcacaga gcacagggnt 150  
cctttttcaa cgtggcgacc agtggccctg accctgctga ctttgtgctt 200  
ggtgtgctgt atagggctgg cagccctggg gcttttgttt tttoagtact 250  
accagctctc caatactggt caagacacca tttctcaaat ggaagaaaaga 300  
ttaggaaata cgtccaaga gttgcaatnt nttcaagtcc agaataataa 350  
gcttgacgga agtntgcagc atgtggctga aaaactctgt cgtgagctgt 400  
atacaaaagc tggaggaaact ttgaaggagg gcaagtntc ctcatntact 450  
atacacacac cacttccc 468

<210> 321  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 321  
atgcaggcca agtacagcag cac 23

<210> 322  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 322  
catgctgacg acttcctgca agc 23

<210> 323  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 323  
ccacacagtc tctgcttctt ggg 23

<210> 324  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 324

atgtctggtatg atgatgggga caccacatg agcctgcatt 40

<210> 325

<211> 2988

<212> DNA

<213> Homo sapiens

<400> 325

gccgagcgca agaaccctgc gcagcccaga gcagctgctg gaggggaatc 50  
gaggcgcggc tcoggggatt cggctcgggc cgtcggtctc gctctgcggg 100  
gagggagcgg gcccgcccg ggggcccgag cctcccgat ccgccccctc 150  
cccggtcccg cccctcggga gactcctctg gctgctctgg gggttcgccg 200  
gggcccggga ccgcgggtcc gggcgccatg cgggcacgc tgctgtgtgc 250  
gggtgtgcgg ccgcagggc ccgtggccgt gggcatctcc ctgggcttca 300  
ccctgagcct gctcagcgc acctgggtgg aggagccgtg cggcccaggc 350  
ccgccccaac ctggagactc tgagctgcgc ccgcgcggca acaccaacgc 400  
ggcgcccgcc ccaactcgg tcagcccgg agcggagcgc gagaagcccg 450  
gggcccggca aggcgcggg gagaattggg agccgcgcgt cttgccctac 500  
cacctgcac agcccggcca ggcgcacaa aaggccgtca ggaccgccta 550  
catcagcacg gagctgggca tcaggcagag gctgctggg gcggtgctga 600  
cctctcagac cagctgccc acgctgggcg tggccgtgaa ccgcacgctg 650  
gggcaccgcg tggagcgtgt ggtgttctc acgggcgcac gggcccgccg 700  
ggccccacct ggcattggcag tggtagcgt gggcgaggag cgaccattg 750  
gacacctgca cctggcgctg cgccacctgc tggagcagca cggcgacgac 800  
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tactgccacg gaggttttg ggtgctgctg tcgcgcatgc tgctgcaaca 1000  
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ggagccagtg caggaggggg acctcattt ccgaagtgcc ctgacagccc 1200  
acctgtgctg tgaccctgtg cacatgtacc agctgcacaa agcttttcgc 1250  
cgagctgaac tggaaacgac gtaccaggag atccaggagt tacagtggga 1300

gatccagaat accagccatc tggccgttga tggggaccgg gcagctgctt 1350  
ggcccgctggg tattccagca ccatcccgcc cggcctcccg ctttgagggtg 1400  
ctgcgctggg actacttcac ggagcagcac gctttctcct gcgccgatgg 1450  
ctcaccocgc tgccactgc gtggggtga ccgggctgat gtggccgatg 1500  
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cggctccaga agcagcagct ggtgaatggc taccgacgct ttgatccggc 1600  
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agccgcgtgg agatcttgcc tgtgccctat gtcactgagg cctcacgtct 1750  
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ccatgcagat gtcttcgcac ctgtcaaggc ccacgtggca gagctggagc 1950  
ggcgcttccc cggtgcccg gtgccatggc tcaagtgtga gacagccgca 2000  
ccctcaccac tgcgcctcat ggatctactc tccaagaagc acccgctgga 2050  
cacactgttc ctgctggcgc gccagacac ggtgctcacg cctgaactcc 2100  
tgaaccgctg ccgcatgcat gccatctccg gctggcaggc cttcttccc 2150  
atgcatttcc aagccttcca ccagggtgtg gccccaccac aaggccctgg 2200  
gccccagag ctgggccgtg aactggccgc ctttgatgc caggcagcca 2250  
gcgaggcctg cttetacaac tcgactacg tggcagccc tgggcgcctg 2300  
gcggcagcct cagaacaaga agaggagctg ctggagagcc tggatgtgta 2350  
cgagctgttc ctocacttct ccagtctgca tgtgctgcgg gcggtggagc 2400  
cggcgctgct gcagcgtac cgggccaga cgtgcagcgc gaggtcagt 2450  
gaggacctgt acoaccgctg cctccagagc gtgcttgagg gcctcggctc 2500  
ccgaaccag ctggccatgc tactcttga acaggagcag ggcaacagca 2550  
cctgacccca ccctgtccc gtgggccgtg gcattggcoac accccacccc 2600  
acttctcccc caaaaccaga gccacctgcc agcctcgtg ggcagggtg 2650  
gcgctagcca gacccaagc tggcccactg gtccctctc tggctctgtg 2700  
ggtccctggg ctctggacaa gcaactgggg acgtgcccc agagccaccc 2750  
acttctcaco ccaaacccag ttccctgcc cctgacgct gctgattcgg 2800  
gctgtggcct ccacgtattt atgcagtaca gtctgcctga cgcagccct 2850  
gcctctgggc cctgggggct gggctgtaga agagtgtgtg gggaaggagg 2900

gagctgagga gggggcatct cccaacttct ccccttttga ccoctgccgaa 2950  
 gctccctgcc ttttaataaac tggccaagtg tggaaaaa 2988

<210> 326  
 <211> 775  
 <212> PRT  
 <213> Homo sapiens

<400> 326  
 Met Arg Ala Ser Leu Leu Leu Ser Val Leu Arg Pro Ala Gly Pro  
 1 5 10 15  
 Val Ala Val Gly Ile Ser Leu Gly Phe Thr Leu Ser Leu Leu Ser  
 20 25 30  
 Val Thr Trp Val Glu Glu Pro Cys Gly Pro Gly Pro Pro Gln Pro  
 35 40 45  
 Gly Asp Ser Glu Leu Pro Pro Arg Gly Asn Thr Asn Ala Ala Arg  
 50 55 60  
 Arg Pro Asn Ser Val Gln Pro Gly Ala Glu Arg Glu Lys Pro Gly  
 65 70 75  
 Ala Gly Glu Gly Ala Gly Glu Asn Trp Glu Pro Arg Val Leu Pro  
 80 85 90  
 Tyr His Pro Ala Gln Pro Gly Gln Ala Ala Lys Lys Ala Val Arg  
 95 100 105  
 Thr Arg Tyr Ile Ser Thr Glu Leu Gly Ile Arg Gln Arg Leu Leu  
 110 115 120  
 Val Ala Val Leu Thr Ser Gln Thr Thr Leu Pro Thr Leu Gly Val  
 125 130 135  
 Ala Val Asn Arg Thr Leu Gly His Arg Leu Glu Arg Val Val Phe  
 140 145 150  
 Leu Thr Gly Ala Arg Gly Arg Arg Ala Pro Gly Met Ala Val  
 155 160 165  
 Val Thr Leu Gly Glu Glu Arg Pro Ile Gly His Leu His Leu Ala  
 170 175 180  
 Leu Arg His Leu Leu Glu Gln His Gly Asp Asp Phe Asp Trp Phe  
 185 190 195  
 Phe Leu Val Pro Asp Thr Thr Tyr Thr Glu Ala His Gly Leu Ala  
 200 205 210  
 Arg Leu Thr Gly His Leu Ser Leu Ala Ser Ala Ala His Leu Tyr  
 215 220 225  
 Leu Gly Arg Pro Gln Asp Phe Ile Gly Gly Glu Pro Thr Pro Gly  
 230 235 240  
 Arg Tyr Cys His Gly Gly Phe Gly Val Leu Leu Ser Arg Met Leu  
 245 250 255  
 Leu Gln Gln Leu Arg Pro His Leu Glu Gly Cys Arg Asn Asp Ile  
 260 265 270

Val Ser Ala Arg	Pro Asp Glu Trp Leu Gly Arg Cys Ile Leu Asp	275	280	285
Ala Thr Gly Val	Gly Cys Thr Gly Asp His Glu Gly Val His Tyr	290	295	300
Ser His Leu Glu	Leu Ser Pro Gly Glu Pro Val Gln Glu Gly Asp	305	310	315
Pro His Phe Arg	Ser Ala Leu Thr Ala His Pro Val Arg Asp Pro	320	325	330
Val His Met Tyr	Gln Leu His Lys Ala Phe Ala Arg Ala Glu Leu	335	340	345
Glu Arg Thr Tyr	Gln Glu Ile Gln Glu Leu Gln Trp Glu Ile Gln	350	355	360
Asn Thr Ser His	Leu Ala Val Asp Gly Asp Arg Ala Ala Ala Trp	365	370	375
Pro Val Gly Ile	Pro Ala Pro Ser Arg Pro Ala Ser Arg Phe Glu	380	385	390
Val Leu Arg Trp	Asp Tyr Phe Thr Glu Gln His Ala Phe Ser Cys	395	400	405
Ala Asp Gly Ser	Pro Arg Cys Pro Leu Arg Gly Ala Asp Arg Ala	410	415	420
Asp Val Ala Asp	Val Leu Gly Thr Ala Leu Glu Glu Leu Asn Arg	425	430	435
Arg Tyr His Pro	Ala Leu Arg Leu Gln Lys Gln Gln Leu Val Asn	440	445	450
Gly Tyr Arg Arg	Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr Leu	455	460	465
Asp Leu Gln Leu	Glu Ala Leu Thr Pro Gln Gly Gly Arg Arg Pro	470	475	480
Leu Thr Arg Arg	Val Gln Leu Leu Arg Pro Leu Ser Arg Val Glu	485	490	495
Ile Leu Pro Val	Pro Tyr Val Thr Glu Ala Ser Arg Leu Thr Val	500	505	510
Leu Leu Pro Leu	Ala Ala Ala Glu Arg Asp Leu Ala Pro Gly Phe	515	520	525
Leu Glu Ala Phe	Ala Thr Ala Ala Leu Glu Pro Gly Asp Ala Ala	530	535	540
Ala Ala Leu Thr	Leu Leu Leu Leu Tyr Glu Pro Arg Gln Ala Gln	545	550	555
Arg Val Ala His	Ala Asp Val Phe Ala Pro Val Lys Ala His Val	560	565	570
Ala Glu Leu Glu	Arg Arg Phe Pro Gly Ala Arg Val Pro Trp Leu	575	580	585

Ser	Val	Gln	Thr	Ala	Ala	Pro	Ser	Pro	Leu	Arg	Leu	Met	Asp	Leu
				590					595					600
Leu	Ser	Lys	Lys	His	Pro	Leu	Asp	Thr	Leu	Phe	Leu	Leu	Ala	Gly
				605					610					615
Pro	Asp	Thr	Val	Leu	Thr	Pro	Asp	Phe	Leu	Asn	Arg	Cys	Arg	Met
				620					625					630
His	Ala	Ile	Ser	Gly	Trp	Gln	Ala	Phe	Phe	Pro	Met	His	Phe	Gln
				635					640					645
Ala	Phe	His	Pro	Gly	Val	Ala	Pro	Pro	Gln	Gly	Pro	Gly	Pro	Pro
				650					655					660
Glu	Leu	Gly	Arg	Asp	Thr	Gly	Arg	Phe	Asp	Arg	Gln	Ala	Ala	Ser
				665					670					675
Glu	Ala	Cys	Phe	Tyr	Asn	Ser	Asp	Tyr	Val	Ala	Ala	Arg	Gly	Arg
				680					685					690
Leu	Ala	Ala	Ala	Ser	Glu	Gln	Glu	Glu	Glu	Leu	Leu	Glu	Ser	Leu
				695					700					705
Asp	Val	Tyr	Glu	Leu	Phe	Leu	His	Phe	Ser	Ser	Leu	His	Val	Leu
				710					715					720
Arg	Ala	Val	Glu	Pro	Ala	Leu	Leu	Gln	Arg	Tyr	Arg	Ala	Gln	Thr
				725					730					735
Cys	Ser	Ala	Arg	Leu	Ser	Glu	Asp	Leu	Tyr	His	Arg	Cys	Leu	Gln
				740					745					750
Ser	Val	Leu	Glu	Gly	Leu	Gly	Ser	Arg	Thr	Gln	Leu	Ala	Met	Leu
				755					760					765
Leu	Phe	Glu	Gln	Glu	Gln	Gly	Asn	Ser	Thr					
				770					775					

<210> 327

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 327

tggaaggctg ccgcaacgac aatc 24

<210> 328

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 328

ctgatgtggc cgaattctg 20

<210> 329

<211> 20

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 329  
 atgggtcagt gtgcagacag 20  
  
 <210> 330  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 330  
 gcatgctgct ccgtgaagta gtcc 24  
  
 <210> 331  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 331  
 atgcatggga aagaaggcct gccc 24  
  
 <210> 332  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 332  
 tgcactggtg accacgaggg ggtgcactat agccatctgg agctgag 47  
  
 <210> 333  
 <211> 1095  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 333  
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 gcctcctctg attggcaagc gctggccacc tccccacacc ccttggaac 100  
 gctcccctag tggagaaaag gagtagctat tagccaattc ggcagggcc 150  
 gctttttaga agcttgattt cctttgaaga tgaagacta gcggaagctc 200  
 tgcctctttc ccagtgggc gagggaaactc ggggcgattg gctgggaact 250  
 gtatccaccc aaatgtcacc gatttcttcc tatgcaggaa atgagcagac 300  
 ccatcaataa gaaattttctc agcctggccg aaaatggttg gccccacgaa 350  
 gccacgacaa ctggaggcaa agagggttgc tcaacgcccc gcctcattgg 400



aaaaccaa at cagatctggg acctatatag cgtggcggag gcggggcgat 450  
 gatttgccg ctcgcaccca ctgcagctgc gcacagtcgc atttctttcc 500  
 ccgcccctga gacctgcag caccatctgt catggcggct ggggtgtttg 550  
 gtttgagcgc tcgccgtctt ttggcggcag cggcgacgcg agggctcccg 600  
 gccgcccgcg tccgctggga atctagcttc tccaggactg tggctgcccc 650  
 gtcgctgtg gcgggaaagc ggccccaga accgaccaca ccgtggcaag 700  
 aggaccaga acccgaggac gaaaacttgt atgagaagaa cccagactcc 750  
 catggttatg acaaggacc cgttttgac gcttggaaca tgcgacttgt 800  
 cttctctttt ggctgtctca tcatctggt ccttggcagc acctttgtgg 850  
 cctatctgcc tgactacagg atgaaagagt ggtcccgcg cgaagctgag 900  
 aggcttgta aataccgaga ggccaatggc ctcccatca tggaatccaa 950  
 ctgcttcgac ccagcaaga tccagctgcc agaggatgag tgaccagttg 1000  
 ctaagtggg ctcaagaagc accgccttcc ccaccccctg cctgccatc 1050  
 tgacctcttc tcagagcacc taattaaagg ggctgaaagt ctgaa 1095

<210> 334

<211> 153

<212> PRT

<213> Homo sapiens

<400> 334

Met	Ala	Ala	Gly	Leu	Phe	Gly	Leu	Ser	Ala	Arg	Arg	Leu	Leu	Ala
1				5					10					15
Ala	Ala	Ala	Thr	Arg	Gly	Leu	Pro	Ala	Ala	Arg	Val	Arg	Trp	Glu
			20					25						30
Ser	Ser	Phe	Ser	Arg	Thr	Val	Val	Ala	Pro	Ser	Ala	Val	Ala	Gly
			35					40						45
Lys	Arg	Pro	Pro	Glu	Pro	Thr	Thr	Pro	Trp	Gln	Glu	Asp	Pro	Glu
			50					55						60
Pro	Glu	Asp	Glu	Asn	Leu	Tyr	Glu	Lys	Asn	Pro	Asp	Ser	His	Gly
			65					70						75
Tyr	Asp	Lys	Asp	Pro	Val	Leu	Asp	Val	Trp	Asn	Met	Arg	Leu	Val
			80					85						90
Phe	Phe	Phe	Gly	Val	Ser	Ile	Ile	Leu	Val	Leu	Gly	Ser	Thr	Phe
			95					100						105
Val	Ala	Tyr	Leu	Pro	Asp	Tyr	Arg	Met	Lys	Glu	Trp	Ser	Arg	Arg
			110					115						120
Glu	Ala	Glu	Arg	Leu	Val	Lys	Tyr	Arg	Glu	Ala	Asn	Gly	Leu	Pro
			125					130						135
Ile	Met	Glu	Ser	Asn	Cys	Phe	Asp	Pro	Ser	Lys	Ile	Gln	Leu	Pro
			140					145						150

Glu Asp Glu

<210> 335  
<211> 442  
<212> DNA  
<213> Homo sapiens

<400> 335  
ggcggctggg ctgtttggtt tgagcgctog cgtottttg gggcagcgg 50  
cgacgcgagg gctcccgcc gcccgctcc gctgggaatc tagcttctcc 100  
aggactgtgg tcgccccgtc cgctgtggcg ggaagcggc cccagaacc 150  
gaccacaccg tggcaagagg accagaacc cgaggacgaa aacttgtagt 200  
agaagaacc agactcccat ggtagtaca aggaccccg tttggacgtc 250  
tggaacatgc gacttgctt ctttttggc gtctccatca tctgggtcct 300  
tggcagcacc tttgtggcct atctgcctga ctacaggatg aaagagtgt 350  
cccgccgca agctgagagg cttgtgaaat accgagaggc caatggcctt 400  
cccatcatgg aatccaactg cttcgacccc agcaagatcc ag 442

<210> 336  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 336  
ctgagaccct gcagacccat ctg 23

<210> 337  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 337  
ggtgttctt gagccccact tagc 24

<210> 338  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 338  
aatctagctt ctccaggact gtggtcgccc cgctcgctgt 40

<210> 339  
<211> 2162  
<212> DNA

<213> Homo sapiens

<400> 339  
gcggcggtcta tgccgcttgc tctgctcgtc ctgttgctcc tggggcccg 50  
cggtcggtgc cttgcagaac ccccacgca cagcctgcgg gaggaacttg 100  
tcatacccc gctgccttcc ggggacgtag ccgccacatt ccagttccgc 150  
acgcgctggg attcggaagt tcagcgggaa ggagtgtccc attacaggct 200  
ctttcccaaa gccctggggc agctgatctc caagtattct ctacggggagc 250  
tgcaactgtc attcacaca ggcttttga ggaccggata ctggggggcca 300  
cccttctcgc agggcccatc aggtgcagag ctgtgggtct ggttccaaga 350  
cactgtcact gatgtggata aatcttgga ggagctcagt aatgtcctct 400  
cagggatctt ctgcgcctct ctcaacttca tcgaactcac caacacagtc 450  
actccactgc cctccttcaa accctgggt ctggccaatg aactgacca 500  
ctactttctg cgtatgtctg tgctgccgcg ggaggtggtc tgcaccgaaa 550  
acctaccccc ctggaagaag ctcttgccct gtatttccaa ggcaggccct 600  
tgtgtgctgc tgaaggcaga tcgcttggtc cacaccagct accactccca 650  
ggcagtgcat atccgccctg tttgcagaaa tgcacgctgt actagcatct 700  
cctgggagct gaggcagacc ctgtcagttg tatttgatgc cttcatcag 750  
gggcaaggaa agaaagactg gtccctcttc cggatgttct cccgaaccct 800  
cacggagccc tgccccctgg cttcagagag ccgagtcctat gtggacatca 850  
ccacctacaa ccaggacaac gagacattag aggtgacccc acccccgacc 900  
actacatata aggacgtcat ctaggcact cggaagacct atgccatcta 950  
tgacttgctt gacacggcca tgatcaacaa ctctcgaaac ctcaacatcc 1000  
agctcaagtg gaagagaccc ccagagaatg agggcccccc agtgcccttc 1050  
ctgcatgccc agcggtagct gagtggctat gggctgcaga agggggagct 1100  
gagcacactg ctgtacaaca cccaccata cggggccttc ccggtgctgc 1150  
tgctggacac cgtaccctgg tatctgcggc tgatatgtca caccctcacc 1200  
atcacctcca agggcaagga gaacaaacca agttacatcc actaccagcc 1250  
tgcccaggac cggctgcaac cccacctct ggagatgctg attcagctgc 1300  
cggccaactc agtcaccaag gtttccatcc agtttgagcg ggcgtgctg 1350  
aagtggacgg agtacacgcc agatcctaac catggcttct atgtcagccc 1400  
atctgtcttc agcgcccttg tgccagcat ggtagcagcc aagccagtgg 1450  
actgggaaga gagtccctc ttcaacagcc tgttccagct ctctgatggc 1500

tctaactact ttgtgcggct ctacacggag cgcgtgctgg tgaacctgcc 1550  
gacaccggac ttcagcatgc cctacaacgt gatctgcctc acgtgcactg 1600  
tggtggccgt gtgctacggc tcctttctaca atctcctcac cgaacacctc 1650  
cacatcgagg agccccgcac aggtggcctg gccaaagcggc tggccaacct 1700  
tatccgggag gcccgagggt tccccccact ctgattcttg ccttttcag 1750  
cagctgcagc tgcggtttct ctctggggag gggagcccaa gggtgtttc 1800  
tgccacttgc tctcctcaga gttggctttt gaaccaaagt gccctggacc 1850  
aggtcagggc ctacagctgt gttgtccagt acaggagcca cgagccaaat 1900  
gtggcatttg aatttgaatt aacttagaaa ttcatttctt cacctgtagt 1950  
ggccacctct atattgaggt gctcaataag caaaagtggc cgggtgctgc 2000  
tgtattggac agcacagaaa aagatttcca tcaccacaga aaggtcggct 2050  
ggcagcactg gccaaaggta tgggggtgtc tacacagtgt atgtcactgt 2100  
gtagtggatg gagtttactg tttgtggaat aaaaacggct gtttcgctgg 2150  
aaaaaaaaaa aa 2162

<210> 340  
<211> 574  
<212> PRT  
<213> Homo sapiens

<400> 340  
Met Pro Leu Ala Leu Leu Val Leu Leu Leu Gly Pro Gly Gly  
1 5 10 15  
Trp Cys Leu Ala Glu Pro Pro Arg Asp Ser Leu Arg Glu Glu Leu  
20 25 30  
Val Ile Thr Pro Leu Pro Ser Gly Asp Val Ala Ala Thr Phe Gln  
35 40 45  
Phe Arg Thr Arg Trp Asp Ser Glu Leu Gln Arg Glu Gly Val Ser  
50 55 60  
His Tyr Arg Leu Phe Pro Lys Ala Leu Gly Gln Leu Ile Ser Lys  
65 70 75  
Tyr Ser Leu Arg Glu Leu His Leu Ser Phe Thr Gln Gly Phe Trp  
80 85 90  
Arg Thr Arg Tyr Trp Gly Pro Pro Phe Leu Gln Ala Pro Ser Gly  
95 100 105  
Ala Glu Leu Trp Val Trp Phe Gln Asp Thr Val Thr Asp Val Asp  
110 115 120  
Lys Ser Trp Lys Glu Leu Ser Asn Val Leu Ser Gly Ile Phe Cys  
125 130 135  
Ala Ser Leu Asn Phe Ile Asp Ser Thr Asn Thr Val Thr Pro Thr  
140 145 150

Ala Ser Phe Lys	Pro Leu Gly Leu Ala	Asn Asp Thr Asp His	Tyr
	155	160	165
Phe Leu Arg Tyr	Ala Val Leu Pro Arg	Glu Val Val Cys Thr	Glu
	170	175	180
Asn Leu Thr Pro	Trp Lys Lys Leu Leu	Pro Cys Ser Ser Lys	Ala
	185	190	195
Gly Leu Ser Val	Leu Leu Lys Ala Asp	Arg Leu Phe His Thr	Ser
	200	205	210
Tyr His Ser Gln	Ala Val His Ile Arg	Pro Val Cys Arg Asn	Ala
	215	220	225
Arg Cys Thr Ser	Ile Ser Trp Glu Leu	Arg Gln Thr Leu Ser	Val
	230	235	240
Val Phe Asp Ala	Phe Ile Thr Gly Gln	Gly Lys Lys Asp Trp	Ser
	245	250	255
Leu Phe Arg Met	Phe Ser Arg Thr Leu	Thr Glu Pro Cys Pro	Leu
	260	265	270
Ala Ser Glu Ser	Arg Val Tyr Val Asp	Ile Thr Thr Tyr Asn	Gln
	275	280	285
Asp Asn Glu Thr	Leu Glu Val His Pro	Pro Thr Thr Thr Tyr	
	290	295	300
Gln Asp Val Ile	Leu Gly Thr Arg Lys	Thr Tyr Ala Ile Tyr	Asp
	305	310	315
Leu Leu Asp Thr	Ala Met Ile Asn Asn	Ser Arg Asn Leu Asn	Ile
	320	325	330
Gln Leu Lys Trp	Lys Arg Pro Pro Glu	Asn Glu Ala Pro Pro	Val
	335	340	345
Pro Phe Leu His	Ala Gln Arg Tyr Val	Ser Gly Tyr Gly Leu	Gln
	350	355	360
Lys Gly Glu Leu	Ser Thr Leu Leu Tyr	Asn Thr His Pro Tyr	Arg
	365	370	375
Ala Phe Pro Val	Leu Leu Leu Asp Thr	Val Pro Trp Tyr Leu	Arg
	380	385	390
Leu Tyr Val His	Thr Leu Thr Ile Thr	Ser Lys Gly Lys Glu	Asn
	395	400	405
Lys Pro Ser Tyr	Ile His Tyr Gln Pro	Ala Gln Asp Arg Leu	Gln
	410	415	420
Pro His Leu Leu	Glu Met Leu Ile Gln	Leu Pro Ala Asn Ser	Val
	425	430	435
Thr Lys Val Ser	Ile Gln Phe Glu Arg	Ala Leu Leu Lys Trp	Thr
	440	445	450
Glu Tyr Thr Pro	Asp Pro Asn His Gly	Phe Thr Val Ser Pro	Ser
	455	460	465

Val	Leu	Ser	Ala	Leu	Val	Pro	Ser	Met	Val	Ala	Ala	Lys	Pro	Val
				470					475					480
Asp	Trp	Glu	Glu	Ser	Pro	Leu	Phe	Asn	Ser	Leu	Phe	Pro	Val	Ser
				485					490					495
Asp	Gly	Ser	Asn	Tyr	Phe	Val	Arg	Leu	Tyr	Thr	Glu	Pro	Leu	Leu
				500					505					510
Val	Asn	Leu	Pro	Thr	Pro	Asp	Phe	Ser	Met	Pro	Tyr	Asn	Val	Ile
				515					520					525
Cys	Leu	Thr	Cys	Thr	Val	Val	Ala	Val	Cys	Tyr	Gly	Ser	Phe	Tyr
				530					535					540
Asn	Leu	Leu	Thr	Arg	Thr	Phe	His	Ile	Glu	Glu	Pro	Arg	Thr	Gly
				545					550					555
Gly	Leu	Ala	Lys	Arg	Leu	Ala	Asn	Leu	Ile	Arg	Arg	Ala	Arg	Gly
				560					565					570

Val Pro Pro Leu

<210> 341  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 341  
 tggacaccgt accctggtat ctgc 24

<210> 342  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic oligonucleotide probe

<400> 342  
 ccaactctga ggagagcaag tggc 24

<210> 343  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 343  
 tgtatgtgca caccctcacc atcacctcca agggcaagga gaac 44

<210> 344  
 <211> 762  
 <212> DNA  
 <213> Homo sapiens

<400> 344  
 caacatgggg tccagcagct tcttggtcct catggtgtct ctcgttcttg 50  
 tgacctgtgt ggctgtggaa ggagttaaag aggttataga gaaagcaggg 100  
 gtttggccag ctgacaacgt acgctgcttc aagtcgatc ctccccagt 150  
 tcacacagac caggactgtc tgggggaaag gaagtgttgt tacctgcact 200  
 gtggcttcaa gtgtgtgatt cctgtgaagg aactggaaga aggaggaaac 250  
 aagatgaag atgtgtcaag gccataacct gagccaggat gggaggccaa 300  
 gtgtccaggc tcctcctcta ccagggtgctc tcagaaatga tgctgggtcc 350  
 tttctacctc tgggggtcac tctcacttgg cacctgcccc tgagggtcct 400  
 gagacttga ataggaaga agcaataccc aacccaccca aagaaaacct 450  
 gagcttgaag tccttttccc caaaaagagg gaagagtcaac aaaaagtcca 500  
 gacccaggg acggtacttt cctctcttac ctggtgctcc tccctaagtc 550  
 tcatgaatgg acccctcatg aatgaaacca gtgccttat aagagacccc 600  
 aaagagctgc cttgccttcc tgcaatgtgt gatcacagct agaaggcact 650  
 gtcagagaag agaaactggt cctcaccaga tgctgaatct gctggtgcct 700  
 tgatcttga cttccagccc tctagaactg taagaaataa atatcttgctg 750  
 tttataatcc aa 762

<210> 345  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 345  
 Met Gly Ser Ser Ser Phe Leu Val Leu Met Val Ser Leu Val Leu  
 1 5 10 15  
 Val Thr Leu Val Ala Val Glu Gly Val Lys Glu Gly Ile Glu Lys  
 20 25 30  
 Ala Gly Val Cys Pro Ala Asp Asn Val Arg Cys Phe Lys Ser Asp  
 35 40 45  
 Pro Pro Gln Cys His Thr Asp Gln Asp Cys Leu Gly Glu Arg Lys  
 50 55 60  
 Cys Cys Tyr Leu His Cys Gly Phe Lys Cys Val Ile Pro Val Lys  
 65 70 75  
 Glu Leu Glu Glu Gly Gly Asn Lys Asp Glu Asp Val Ser Arg Pro  
 80 85 90  
 Tyr Pro Glu Pro Gly Trp Glu Ala Lys Cys Pro Gly Ser Ser Ser  
 95 100 105  
 Thr Arg Cys Pro Gln Lys  
 110

<210> 346  
 <211> 2528  
 <212> DNA  
 <213> Homo sapiens

<400> 346  
 aaactcagca cttgccggag tggctcattg ttaagacaaa ggggtgtgcac 50  
 ttctctggcca ggaacacctga gcggtgagac tcccagctgc ctacatcaag 100  
 gcccacaggac atgoagaacc ttctctotaga acccgaccca ccaccatgag 150  
 gtctctcctg tggagatgca ggcacctgag ccaaggcgtc cagtggctcct 200  
 tgccttctggc tgtcctggtc ttctttctct tgccttgcc ctcttttatt 250  
 aaggagcctc aaacaaagcc ttccaggcat caacgcacag agaacattaa 300  
 agaaaggctc ctacagtccc tggcaaagcc taagtcccag gacccacaa 350  
 gggcgaggag gacaaccatc tatgcagagc cagcgccaga gaacaatgcc 400  
 ctcaacacac aaacccagcc caaggccac accacggag acagaggaaa 450  
 ggaggccaac caggcacccg cggaggagca ggacaagggt ccccacacag 500  
 cacagagggc agcatggaag agcccagaaa aagagaaaac catggtgaac 550  
 aactgtcac ccagagggca agatgcaggg atggcctctg gcaggacaga 600  
 ggcacaatca tggaaagacc aggacacaaa gacgaccaa ggaaatggg 650  
 gccagaccag gaagctgacg gcctccagga cgggtgcaga gaagcaccag 700  
 ggcaaagcgg caaccacagc caagacgctc attcccaaaa gtcagcacag 750  
 aatgctggct cccacaggag cagtgtcaac aaggacgaga cagaaaggag 800  
 tgaccacagc agtcatcca cctaaggaga agaaacctca ggccaccca 850  
 cccctgccc ctttccagag cccacgacg cagagaaaac aaagactgaa 900  
 ggccgccaac ttcaaatctg agcctcgggt ggattttgag gaaaaataca 950  
 gcttogaat aggaggcctt cagacgactt gccctgactc tgtgaagatc 1000  
 aaagcctcca agtcgctgtg gctccagaaa ctctttctgc ccaacctcac 1050  
 tctcttctg gactccagac acttcaacca gagtgtgtgg gaccgccttg 1100  
 aacactttgc accacccttt ggcttcattg agctcaacta ctcttgggtg 1150  
 cagaaggctg tgacacgctt ccctccagt cccagcagc agctgtcct 1200  
 ggccagcctc ccgctggga gcctccggtg catcacctgt gccgtggtg 1250  
 gcaacggggg catcctgaac aactcccaca tgggccagga gatagacagt 1300  
 cagactacg tgttccgatt gagcggagct ctcatataag gctacgaaca 1350  
 ggatgtggg actcggacat ccttctacg ctttaccgc ttctccctga 1400  
 cccagtcact ctttatattg ggcaatcggg gtttcaagaa cgtgcctctt 1450



gggaaggacg tccgctactt gcacttctctg gaaggcaccg gggactatga 1500  
 gtggctggaa gcactgctta tgaatcagac ggtgatgtca aaaaaccttt 1550  
 tctggttcag gcacagaccc caggaagctt ttccgggaagc cctgcacatg 1600  
 gacaggtacc tggtgtgca cccagacttt ctccgataca tgaagaacag 1650  
 gtttctgagg tctaagaccc tggatggtgc ccaactggagg atataccgcc 1700  
 ccaccactgg ggccctctctg ctgctcactg cccttcagct ctgtgaccag 1750  
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 ctactatgat acatcatgga agcggctgat cttttacata aacctgact 1850  
 tcaagctgga gagagaagtc tggaagcggc tacacgatga agggataatc 1900  
 cggtctgacc agcgtctctg tcccggaact gccaaagcca agaactgacc 1950  
 ggggccaggg ctgccatggt ctccctgcct gctccaaggc acaggataca 2000  
 gtgggaatct tgagactctt tggccatttc ccatggctca gactaagctc 2050  
 caagcccttc aggagtcca agggaacact tgaacctagg acaagactct 2100  
 ctcaagatgg caaatggcta attgagggtc tgaagtctct cagtacattg 2150  
 ctgtaggctc tgaggccagg gatttttaac taaatggggt gatgggtggc 2200  
 caataccaca attctgctg aaaaacactc ttccagtcca aaagcttctt 2250  
 gatacagaaa aaagagcctg gatttacaga aacatataga tctggtttga 2300  
 attccagatc gagtttacg ttgtgaaatc ttgaaggtat tacttaactt 2350  
 cactacagat tgtctagaag acctttctag gagttatctg attctagaag 2400  
 ggtctatact tgtccttgtc tttaagctat ttgacaactc tacgtgttgt 2450  
 agaaaaactg taataataca aatgattggt gtccatggaa aggcaataa 2500  
 attttctaca gtgaaaaaaaa aaaaaaaa 2528

<210> 347

<211> 600

<212> PRT

<213> Homo sapiens

<400> 347

Met	Arg	Ser	Cys	Leu	Trp	Arg	Cys	Arg	His	Leu	Ser	Gln	Gly	Val
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Gln	Trp	Ser	Leu	Leu	Ala	Val	Leu	Val	Phe	Phe	Leu	Phe	Ala	
			20					25					30	

Leu	Pro	Ser	Phe	Ile	Lys	Glu	Pro	Gln	Thr	Lys	Pro	Ser	Arg	His
			35						40				45	

Gln	Arg	Thr	Glu	Asn	Ile	Lys	Glu	Arg	Ser	Leu	Gln	Ser	Leu	Ala
			50						55				60	

Lys	Pro	Lys	Ser	Gln	Ala	Pro	Thr	Arg	Ala	Arg	Arg	Thr	Thr	Ile
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

65										70					75				
Tyr	Ala	Glu	Pro	Ala	Pro	Glu	Asn	Asn	Ala	Leu	Asn	Thr	Gln	Thr					
				80					85					90					
Gln	Pro	Lys	Ala	His	Thr	Thr	Gly	Asp	Arg	Gly	Lys	Glu	Ala	Asn					
				95					100					105					
Gln	Ala	Pro	Pro	Glu	Glu	Gln	Asp	Lys	Val	Pro	His	Thr	Ala	Gln					
				110					115					120					
Arg	Ala	Ala	Trp	Lys	Ser	Pro	Glu	Lys	Glu	Lys	Thr	Met	Val	Asn					
				125					130					135					
Thr	Leu	Ser	Pro	Arg	Gly	Gln	Asp	Ala	Gly	Met	Ala	Ser	Gly	Arg					
				140					145					150					
Thr	Glu	Ala	Gln	Ser	Trp	Lys	Ser	Gln	Asp	Thr	Lys	Thr	Thr	Gln					
				155					160					165					
Gly	Asn	Gly	Gly	Gln	Thr	Arg	Lys	Leu	Thr	Ala	Ser	Arg	Thr	Val					
				170					175					180					
Ser	Glu	Lys	His	Gln	Gly	Lys	Ala	Ala	Thr	Thr	Ala	Lys	Thr	Leu					
				185					190					195					
Ile	Pro	Lys	Ser	Gln	His	Arg	Met	Leu	Ala	Pro	Thr	Gly	Ala	Val					
				200					205					210					
Ser	Thr	Arg	Thr	Arg	Gln	Lys	Gly	Val	Thr	Thr	Ala	Val	Ile	Pro					
				215					220					225					
Pro	Lys	Glu	Lys	Lys	Pro	Gln	Ala	Thr	Pro	Pro	Pro	Ala	Pro	Phe					
				230					235					240					
Gln	Ser	Pro	Thr	Thr	Gln	Arg	Asn	Gln	Arg	Leu	Lys	Ala	Ala	Asn					
				245					250					255					
Phe	Lys	Ser	Glu	Pro	Arg	Trp	Asp	Phe	Glu	Glu	Lys	Tyr	Ser	Phe					
				260					265					270					
Glu	Ile	Gly	Gly	Leu	Gln	Thr	Thr	Cys	Pro	Asp	Ser	Val	Lys	Ile					
				275					280					285					
Lys	Ala	Ser	Lys	Ser	Leu	Trp	Leu	Gln	Lys	Leu	Phe	Leu	Pro	Asn					
				290					295					300					
Leu	Thr	Leu	Phe	Leu	Asp	Ser	Arg	His	Phe	Asn	Gln	Ser	Glu	Trp					
				305					310					315					
Asp	Arg	Leu	Glu	His	Phe	Ala	Pro	Pro	Phe	Gly	Phe	Met	Glu	Leu					
				320					325					330					
Asn	Tyr	Ser	Leu	Val	Gln	Lys	Val	Val	Thr	Arg	Phe	Pro	Pro	Val					
				335					340					345					
Pro	Gln	Gln	Gln	Leu	Leu	Leu	Ala	Ser	Leu	Pro	Ala	Gly	Ser	Leu					
				350					355					360					
Arg	Cys	Ile	Thr	Cys	Ala	Val	Val	Gly	Asn	Gly	Gly	Ile	Leu	Asn					
				365					370					375					
Asn	Ser	His	Met	Gly	Gln	Glu	Ile	Asp	Ser	His	Asp	Tyr	Val	Phe					

380	385	390
Arg Leu Ser Gly	Ala Leu Ile Lys Gly	Tyr Glu Gln Asp Val Gly
395	400	405
Thr Arg Thr Ser	Phe Tyr Gly Phe Thr	Ala Phe Ser Leu Thr Gln
410	415	420
Ser Leu Leu Ile	Leu Gly Asn Arg Gly	Phe Lys Asn Val Pro Leu
425	430	435
Gly Lys Asp Val	Arg Tyr Leu His Phe	Leu Glu Gly Thr Arg Asp
440	445	450
Tyr Glu Trp Leu	Glu Ala Leu Leu Met	Asn Gln Thr Val Met Ser
455	460	465
Lys Asn Leu Phe	Trp Phe Arg His Arg	Pro Gln Glu Ala Phe Arg
470	475	480
Glu Ala Leu His	Met Asp Arg Tyr Leu	Leu Leu His Pro Asp Phe
485	490	495
Leu Arg Tyr Met	Lys Asn Arg Phe Leu	Arg Ser Lys Thr Leu Asp
500	505	510
Gly Ala His Trp	Arg Ile Tyr Arg Pro	Thr Thr Gly Ala Leu Leu
515	520	525
Leu Leu Thr Ala	Leu Gln Leu Cys Asp	Gln Val Ser Ala Tyr Gly
530	535	540
Phe Ile Thr Glu	Gly His Glu Arg Phe	Ser Asp His Tyr Tyr Asp
545	550	555
Thr Ser Trp Lys	Arg Leu Ile Phe Tyr	Ile Asn His Asp Phe Lys
560	565	570
Leu Glu Arg Glu	Val Trp Lys Arg Leu	His Asp Glu Gly Ile Ile
575	580	585
Arg Leu Tyr Gln	Arg Pro Gly Pro Gly	Thr Ala Lys Ala Lys Asn
590	595	600

<210> 348

<211> 496

<212> DNA

<213> Homo sapiens

<400> 348

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agtgcagcaa acacttccat agactttatc acaacaccag agactgcacc 200

attcctgcat actataaaag atgcgccagg cttottaccc ggctggctgt 250

cagtccagtg tgcattggagg ataagtgagc agaccgtaca ggagcagcac 300

accaggagcc atgagaagtg ccttggaaac caacagggaa acagaactat 350

ctttatacac atccccctcat ggacaagaga tttatttttg cagacagact 400  
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 <211> 91  
 <212> PRT  
 <213> Homo sapiens

<400> 349  
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 35 40 45  
 Tyr Phe Ser Pro Lys Cys Ser Lys His Phe His Arg Leu Tyr His  
 50 55 60  
 Asn Thr Arg Asp Cys Thr Ile Pro Ala Tyr Tyr Lys Arg Cys Ala  
 65 70 75  
 Arg Leu Leu Thr Arg Leu Ala Val Ser Pro Val Cys Met Glu Asp  
 80 85 90  
 Lys

<210> 350  
 <211> 1141  
 <212> DNA  
 <213> Homo sapiens

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 caggcatcgc etcagctgtg atcctctttg ttgctgtggt tgccaccacc 400  
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 tgcagccagt ataccatac cccagggacc ccaaagctgg ccttgcccc 550  
 ccacagcctg gcttcatgta cccacctagt ggtcctgctc cccaatatcc 600

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<210> 351

<211> 197

<212> PRT

<213> Homo sapiens

<400> 351

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			20						25					30
Cys	Leu	Trp	Tyr	Leu	Asp	Arg	Asn	Gly	Ser	Trp	His	Pro	Gly	Phe
			35						40					45
Asn	Cys	Glu	Phe	Phe	Thr	Phe	Cys	Cys	Gly	Thr	Cys	Tyr	His	Arg
			50						55					60
Tyr	Cys	Cys	Arg	Asp	Leu	Thr	Leu	Leu	Ile	Thr	Glu	Arg	Gln	Gln
			65						70					75
Lys	His	Cys	Leu	Ala	Phe	Ser	Pro	Lys	Thr	Ile	Ala	Gly	Ile	Ala
			80						85					90
Ser	Ala	Val	Ile	Leu	Phe	Val	Ala	Val	Val	Ala	Thr	Thr	Ile	Cys
			95						100					105
Cys	Phe	Leu	Cys	Ser	Cys	Cys	Tyr	Leu	Tyr	Arg	Arg	Arg	Gln	Gln
			110						115					120
Leu	Gln	Ser	Pro	Phe	Glu	Gly	Gln	Glu	Ile	Pro	Met	Thr	Gly	Ile
			125						130					135
Pro	Val	Gln	Pro	Val	Tyr	Pro	Tyr	Pro	Gln	Asp	Pro	Lys	Ala	Gly
			140						145					150
Pro	Ala	Pro	Pro	Gln	Pro	Gly	Phe	Met	Tyr	Pro	Pro	Ser	Gly	Pro
			155						160					165
Ala	Pro	Gln	Tyr	Pro	Leu	Tyr	Pro	Ala	Gly	Pro	Pro	Val	Tyr	Asn
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Pro Ala Ala Pro Pro Pro Tyr Met Pro Pro Gln Pro Ser Tyr Pro  
185 190 195

Gly Ala

<210> 352  
<211> 3226  
<212> DNA  
<213> Homo sapiens

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tctotttaact gtgtccactc ctctcatggtg tcagagcact gaagcatctc 200  
caaaacgtag tgatgggaca ccatttcctt ggaataaaa acgacttcct 250  
gagtacgtca tcccagttca ttatgatctc ttgatccatg caaaccttac 300  
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ccaccagcac catcatcctg catagtcacc acctgcagat atctagggcc 400  
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gcccaccagt ggtttgggaa cctggtoact atggaatggt ggaatgatct 1200  
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<210> 353  
 <211> 941  
 <212> PRT  
 <213> Homo sapiens

<400> 353  
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 Trp Cys Gln Ser Thr Glu Ala Ser Pro Lys Arg Ser Asp Gly Thr  
 35 40 45  
 Pro Phe Pro Trp Asn Lys Ile Arg Leu Pro Glu Tyr Val Ile Pro  
 50 55 60  
 Val His Tyr Asp Leu Leu Ile His Ala Asn Leu Thr Thr Leu Thr  
 65 70 75  
 Phe Trp Gly Thr Thr Lys Val Glu Ile Thr Ala Ser Gln Pro Thr  
 80 85 90  
 Ser Thr Ile Ile Leu His Ser His His Leu Gln Ile Ser Arg Ala  
 95 100 105  
 Thr Leu Arg Lys Gly Ala Gly Glu Arg Leu Ser Glu Glu Pro Leu  
 110 115 120  
 Gln Val Leu Glu His Pro Pro Gln Glu Gln Ile Ala Leu Leu Ala  
 125 130 135  
 Pro Glu Pro Leu Leu Val Gly Leu Pro Tyr Thr Val Val Ile His  
 140 145 150  
 Tyr Ala Gly Asn Leu Ser Glu Thr Phe His Gly Phe Tyr Lys Ser  
 155 160 165  
 Thr Tyr Arg Thr Lys Glu Gly Glu Leu Arg Ile Leu Ala Ser Thr  
 170 175 180  
 Gln Phe Glu Pro Thr Ala Ala Arg Met Ala Phe Pro Cys Phe Asp  
 185 190 195  
 Glu Pro Ala Phe Lys Ala Ser Phe Ser Ile Lys Ile Arg Arg Glu  
 200 205 210  
 Pro Arg His Leu Ala Ile Ser Asn Met Pro Leu Val Lys Ser Val



	215		220		225
Thr Val Ala Glu Gly Leu Ile Glu Asp His Phe Asp Val Thr Val	230		235		240
Lys Met Ser Thr Tyr Leu Val Ala Phe Ile Ile Ser Asp Phe Glu	245		250		255
Ser Val Ser Lys Ile Thr Lys Ser Gly Val Lys Val Ser Val Tyr	260		265		270
Ala Val Pro Asp Lys Ile Asn Gln Ala Asp Tyr Ala Leu Asp Ala	275		280		285
Ala Val Thr Leu Leu Glu Phe Tyr Glu Asp Tyr Phe Ser Ile Pro	290		295		300
Tyr Pro Leu Pro Lys Gln Asp Leu Ala Ala Ile Pro Asp Phe Gln	305		310		315
Ser Gly Ala Met Glu Asn Trp Gly Leu Thr Thr Tyr Arg Glu Ser	320		325		330
Ala Leu Leu Phe Asp Ala Glu Lys Ser Ser Ala Ser Ser Lys Leu	335		340		345
Gly Ile Thr Val Thr Val Ala His Glu Leu Ala His Gln Trp Phe	350		355		360
Gly Asn Leu Val Thr Met Glu Trp Trp Asn Asp Leu Trp Leu Asn	365		370		375
Glu Gly Phe Ala Lys Phe Met Glu Phe Val Ser Val Ser Val Thr	380		385		390
His Pro Glu Leu Lys Val Gly Asp Tyr Phe Phe Gly Lys Cys Phe	395		400		405
Asp Ala Met Glu Val Asp Ala Leu Asn Ser Ser His Pro Val Ser	410		415		420
Thr Pro Val Glu Asn Pro Ala Gln Ile Arg Glu Met Phe Asp Asp	425		430		435
Val Ser Tyr Asp Lys Gly Ala Cys Ile Leu Asn Met Leu Arg Glu	440		445		450
Tyr Leu Ser Ala Asp Ala Phe Lys Ser Gly Ile Val Gln Tyr Leu	455		460		465
Gln Lys His Ser Tyr Lys Asn Thr Lys Asn Glu Asp Leu Trp Asp	470		475		480
Ser Met Ala Ser Ile Cys Pro Thr Asp Gly Val Lys Gly Met Asp	485		490		495
Gly Phe Cys Ser Arg Ser Gln His Ser Ser Ser Ser His Trp	500		505		510
His Gln Glu Gly Val Asp Val Lys Thr Met Met Asn Thr Trp Thr	515		520		525
Leu Gln Arg Gly Phe Pro Leu Ile Thr Ile Thr Val Arg Gly Arg					

	530		535		540
Asn Val His Met	Lys Gln Glu His Tyr	Met Lys Gly Ser Asp Gly			
	545	550			555
Ala Pro Asp Thr	Gly Tyr Leu Trp His	Val Pro Leu Thr Phe Ile			
	560	565			570
Thr Ser Lys Ser	Asn Met Val His Arg	Phe Leu Leu Lys Thr Lys			
	575	580			585
Thr Asp Val Leu	Ile Leu Pro Glu Glu	Val Glu Trp Ile Lys Phe			
	590	595			600
Asn Val Gly Met	Asn Gly Tyr Tyr Ile	Val His Tyr Glu Asp Asp			
	605	610			615
Gly Trp Asp Ser	Leu Thr Gly Leu Leu Lys	Gly Thr His Thr Ala			
	620	625			630
Val Ser Ser Asn	Asp Arg Ala Ser Leu	Ile Asn Asn Ala Phe Gln			
	635	640			645
Leu Val Ser Ile	Gly Lys Leu Ser Ile	Glu Lys Ala Leu Asp Leu			
	650	655			660
Ser Leu Tyr Leu	Lys His Glu Thr Glu	Ile Met Pro Val Phe Gln			
	665	670			675
Gly Leu Asn Glu	Leu Ile Pro Met Tyr	Lys Leu Met Glu Lys Arg			
	680	685			690
Asp Met Asn Glu	Val Glu Thr Gln Phe	Lys Ala Phe Leu Ile Arg			
	695	700			705
Leu Leu Arg Asp	Leu Ile Asp Lys Gln	Thr Trp Thr Asp Glu Gly			
	710	715			720
Ser Val Ser Glu	Gln Met Leu Arg Ser	Glu Leu Leu Leu Ala			
	725	730			735
Cys Val His Asn	Tyr Gln Pro Cys Val	Gln Arg Ala Glu Gly Tyr			
	740	745			750
Phe Arg Lys Trp	Lys Glu Ser Asn Gly	Asn Leu Ser Leu Pro Val			
	755	760			765
Asp Val Thr Leu	Ala Val Phe Ala Val	Gly Ala Gln Ser Thr Glu			
	770	775			780
Gly Trp Asp Phe	Leu Tyr Ser Lys Tyr	Gln Phe Ser Leu Ser Ser			
	785	790			795
Thr Glu Lys Ser	Gln Ile Glu Phe Ala	Leu Cys Arg Thr Gln Asn			
	800	805			810
Lys Glu Lys Leu	Gln Trp Leu Leu Asp	Glu Ser Phe Lys Gly Asp			
	815	820			825
Lys Ile Lys Thr	Gln Glu Phe Pro Gln	Ile Leu Thr Leu Ile Gly			
	830	835			840
Arg Asn Pro Val	Gly Tyr Pro Leu Ala	Trp Gln Phe Leu Arg Lys			

	845		850		855
Asn Trp Asn Lys	Leu Val Gln Lys Phe	Glu Leu Gly Ser Ser Ser			
	860	865			870
Ile Ala His Met	Val Met Gly Thr Thr	Asn Gln Phe Ser Thr Arg			
	875	880			885
Thr Arg Leu Glu	Glu Val Lys Gly Phe	Phe Ser Ser Leu Lys Glu			
	890	895			900
Asn Gly Ser Gln	Leu Arg Cys Val Gln	Gln Thr Ile Glu Thr Ile			
	905	910			915
Glu Glu Asn Ile	Gly Trp Met Asp Lys	Asn Phe Asp Lys Ile Arg			
	920	925			930
Val Trp Leu Gln	Ser Glu Lys Leu Glu Arg Met				
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<210> 354  
 <211> 1587  
 <212> DNA  
 <213> Homo sapiens

<400> 354  
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 gttcagcatg tgtggaaggt gtcgcaccta ccccggaat ggaccctaa 150  
 gaacaccagc tgcgacagcg gcttgggggtg ccaggacacg ttgatgctca 200  
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 gccaaaggacc aggagccccg cgtcactgag caccggatgg gccccggcct 300  
 ctccctgata tctacacct tcgtgtgccg ccaggaggac ttctgcaaca 350  
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 aatggccttg gacaccagat tctttcccat totgtccatg aatcatcttc 1450  
 cccacacaca atcattcata totactcacc taacagcaac actggggaga 1500  
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<210> 355

<211> 437

<212> PRT

<213> Homo sapiens

<400> 355

Met	Ser	Ala	Val	Leu	Leu	Leu	Ala	Leu	Leu	Gly	Phe	Ile	Leu	Pro
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Leu	Pro	Gly	Val	Gln	Ala	Leu	Leu	Cys	Gln	Phe	Gly	Thr	Val	Gln
				20						25				30
His	Val	Trp	Lys	Val	Ser	Asp	Leu	Pro	Arg	Gln	Trp	Thr	Pro	Lys
				35						40				45
Asn	Thr	Ser	Cys	Asp	Ser	Gly	Leu	Gly	Cys	Gln	Asp	Thr	Leu	Met
				50						55				60
Leu	Ile	Glu	Ser	Gly	Pro	Gln	Val	Ser	Leu	Val	Leu	Ser	Lys	Gly
				65						70				75
Cys	Thr	Glu	Ala	Lys	Asp	Gln	Glu	Pro	Arg	Val	Thr	Glu	His	Arg
				80						85				90
Met	Gly	Pro	Gly	Leu	Ser	Leu	Ile	Ser	Tyr	Thr	Phe	Val	Cys	Arg
				95						100				105
Gln	Glu	Asp	Phe	Cys	Asn	Asn	Leu	Val	Asn	Ser	Leu	Pro	Leu	Trp
				110						115				120
Ala	Pro	Gln	Pro	Pro	Ala	Asp	Pro	Gly	Ser	Leu	Arg	Cys	Pro	Val
				125						130				135
Cys	Leu	Ser	Met	Glu	Gly	Cys	Leu	Glu	Gly	Thr	Thr	Glu	Glu	Ile
				140						145				150
Cys	Pro	Lys	Gly	Thr	Thr	His	Cys	Tyr	Asp	Gly	Leu	Leu	Arg	Leu

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Arg Gly Gly Gly Ile Phe Ser Asn Leu	Arg Val Gln Gly Cys Met	
170	175	180
Pro Gln Pro Gly Cys Asn Leu Leu Asn Gly Thr Gln Glu Ile Gly		
185	190	195
Pro Val Gly Met Thr Glu Asn Cys Asn Arg Lys Asp Phe Leu Thr		
200	205	210
Cys His Arg Gly Thr Thr Ile Met Thr His Gly Asn Leu Ala Gln		
215	220	225
Glu Pro Thr Asp Trp Thr Thr Ser Asn Thr Glu Met Cys Glu Val		
230	235	240
Gly Gln Val Cys Gln Glu Thr Leu Leu Leu Ile Asp Val Gly Leu		
245	250	255
Thr Ser Thr Leu Val Gly Thr Lys Gly Cys Ser Thr Val Gly Ala		
260	265	270
Gln Asn Ser Gln Lys Thr Thr Ile His Ser Ala Pro Pro Gly Val		
275	280	285
Leu Val Ala Ser Tyr Thr His Phe Cys Ser Ser Asp Leu Cys Asn		
290	295	300
Ser Ala Ser Ser Ser Ser Val Leu Leu Asn Ser Leu Pro Pro Gln		
305	310	315
Ala Ala Pro Val Pro Gly Asp Arg Gln Cys Pro Thr Cys Val Gln		
320	325	330
Pro Leu Gly Thr Cys Ser Ser Gly Ser Pro Arg Met Thr Cys Pro		
335	340	345
Arg Gly Ala Thr His Cys Tyr Asp Gly Tyr Ile His Leu Ser Gly		
350	355	360
Gly Gly Leu Ser Thr Lys Met Ser Ile Gln Gly Cys Val Ala Gln		
365	370	375
Pro Ser Ser Phe Leu Leu Asn His Thr Arg Gln Ile Gly Ile Phe		
380	385	390
Ser Ala Arg Glu Lys Arg Asp Val Gln Pro Pro Ala Ser Gln His		
395	400	405
Glu Gly Gly Gly Ala Glu Gly Leu Glu Ser Leu Thr Trp Gly Val		
410	415	420
Gly Leu Ala Leu Ala Pro Ala Leu Trp Trp Gly Val Val Cys Pro		
425	430	435
Ser Cys		

<210> 356  
 <211> 1238  
 <212> DNA  
 <213> Homo sapiens

<400> 356  
 gcgacgggga ggacgccccg ttgcctagc gcgtgctcag gagttggtgt 50  
 cctgcctgcg ctcaggatga gggggaatct ggccctggtg ggcgttctaa 100  
 tcagcctggc cttcctgtca ctgctgccat ctggacatcc tcagccggct 150  
 ggcatgacg cctgctctgt gcagatcctc gtccttgccc tcaaagggga 200  
 tgccggagag aaggagagaca aaggcggccc cggacggcct ggaagagtcg 250  
 gcccacggg agaaaaagga gacatggggg acaaaggaca gaaaggcagt 300  
 gtgggtcgtc atggaaaaat tgggtccatt ggcctctaaag gtgagaaagg 350  
 agattccggt gacataggac cccctgggtcc taatggagaa ccaggcctcc 400  
 catgtgagtg cagccagctg cgcaaggcca tcggggagat ggacaaccag 450  
 gtctctcagc tgaccagcga gctcaagttc atcaagaatg ctgtgcgcgg 500  
 tgtgcgcgag acggagagca agatctacct gctggtgaag gaggagaagc 550  
 gctacgcgga cgcccagctg tcctgccagg gccgcggggg cacgctgagc 600  
 atgcccaagg acgaggctgc caatggcctg atggccgcat acctggcgca 650  
 agccggcctg gcccggtgtc tcacatggcat caacgacctg gagaaggagg 700  
 gcgccttcgt gtactctgac cactccccc a tcgggacctt caacaagtgg 750  
 cgcagcgggt agcccaacaa tgctacgac gaggaggact gcgtggagat 800  
 ggtggcctcg ggcggtgga acgacgtggc ctgccacacc acctgtact 850  
 tcattgtgtg gtttgacaag gagaacatgt gaggcctagg ctggggctgc 900  
 ccattggggg ccccatatgt ccctgcaggg ttggcaggga cagagcccag 950  
 accatggtgc cagccaggga gctgtccctc tgtgaagggt ggaggctcac 1000  
 tgagtagagg gctgttgtct aaactgagaa aatggcctat gcttaagagg 1050  
 aaaatgaaa tggtcctggg gtgctgtctc tgaagaagca gagtttcatt 1100  
 acctgtattg tagccccaat gtcattatgt aattattacc cagaattgct 1150  
 cttccataaa gcttgtgctt ttgtccaagc tatacaataa aatctttaag 1200  
 tagtgacgta gttaagtcca aaaaaaaaaa aaaaaaaaa 1238

<210> 357  
 <211> 271  
 <212> PRT  
 <213> Homo sapiens

<400> 357  
 Met Arg Gly Asn Leu Ala Leu Val Gly Val Leu Ile Ser Leu Ala  
 1 5 10 15  
 Phe Leu Ser Leu Leu Pro Ser Gly His Pro Gln Pro Ala Gly Asp  
 20 25 30

Asp	Ala	Cys	Ser	Val	Gln	Ile	Leu	Val	Pro	Gly	Leu	Lys	Gly	Asp	
				35					40					45	
Ala	Gly	Glu	Lys	Gly	Asp	Lys	Gly	Ala	Pro	Gly	Arg	Pro	Gly	Arg	
				50					55					60	
Val	Gly	Pro	Thr	Gly	Glu	Lys	Gly	Asp	Met	Gly	Asp	Lys	Gly	Gln	
				65					70					75	
Lys	Gly	Ser	Val	Gly	Arg	His	Gly	Lys	Ile	Gly	Pro	Ile	Gly	Ser	
				80					85					90	
Lys	Gly	Glu	Lys	Gly	Asp	Ser	Gly	Asp	Ile	Gly	Pro	Pro	Gly	Pro	
				95					100					105	
Asn	Gly	Glu	Pro	Gly	Leu	Pro	Cys	Glu	Cys	Ser	Gln	Leu	Arg	Lys	
				110					115					120	
Ala	Ile	Gly	Glu	Met	Asp	Asn	Gln	Val	Ser	Gln	Leu	Thr	Ser	Glu	
				125					130					135	
Leu	Lys	Phe	Ile	Lys	Asn	Ala	Val	Ala	Gly	Val	Arg	Glu	Thr	Glu	
				140					145					150	
Ser	Lys	Ile	Tyr	Leu	Leu	Val	Lys	Glu	Glu	Lys	Arg	Tyr	Ala	Asp	
				155					160					165	
Ala	Gln	Leu	Ser	Cys	Gln	Gly	Arg	Gly	Gly	Thr	Leu	Ser	Met	Pro	
				170					175					180	
Lys	Asp	Glu	Ala	Ala	Asn	Gly	Leu	Met	Ala	Ala	Tyr	Leu	Ala	Gln	
				185					190					195	
Ala	Gly	Leu	Ala	Arg	Val	Phe	Ile	Gly	Ile	Asn	Asp	Leu	Glu	Lys	
				200					205					210	
Glu	Gly	Ala	Phe	Val	Tyr	Ser	Asp	His	Ser	Pro	Met	Arg	Thr	Phe	
				215					220					225	
Asn	Lys	Trp	Arg	Ser	Gly	Glu	Pro	Asn	Asn	Ala	Tyr	Asp	Glu	Glu	
				230					235					240	
Asp	Cys	Val	Glu	Met	Val	Ala	Ser	Gly	Gly	Trp	Asn	Asp	Val	Ala	
				245					250					255	
Cys	His	Thr	Thr	Met	Tyr	Phe	Met	Cys	Glu	Phe	Asp	Lys	Glu	Asn	
				260					265					270	

Met

<210> 358  
 <211> 972  
 <212> DNA  
 <213> Homo sapiens

<400> 358  
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 gagcaccggc agcaccagtg tgtgaggggga gcaggcagcg gtcctagcca 100  
 gttccttgat cctgccagac caccagccc ccggcacaga gctgctccac 150

aggcaccatg aggatcatgc tgctattcac agccatcctg gccttcagcc 200  
tagctcagag ctttggggct gtctgtaagg agccacagga ggagggtgtt 250  
cctggcgggg gccgcagcaa gagggatcca gatctctacc agctgctcca 300  
gagactcttc aaaagccact catctctgga gggattgctc aaagccctga 350  
gccaggctag cacagatcct aaggaatcaa catctcccga gaaacgtgac 400  
atgcatgact tctttgtggg acttatgggc aagaggagcg tccagccaga 450  
gggaagaca ggacctttct taccttcagt gaggttctc cgcccccttc 500  
atcccaatca gcttgatoc acaggaagt ctccctggg aacagaggag 550  
cagagacctt tataagactc tctacggat gtgaatcaag agaacgtccc 600  
cagctttggc atctcaagt atccccgag agcagaatag gtactccact 650  
tccggactcc tggactgcat taggaagacc tctttccctg tcccaatccc 700  
caggtgcgca cgctcctgtt accctttctc ttcctgttc ttgtaacatt 750  
cttgtgcttt gactccttct ccatcttttc tacctgacct tgggtgtgaa 800  
actgcatagt gaatatcccc aaccccaatg ggcatgact gtagaatacc 850  
ctagagtcc tgtagtgtcc tacattaaaa atataatgct tctctctatt 900  
cctcaacaat aaaggatttt tgcatatgaa aaaaaaaaa aaaaaaaaa 950  
aaaaaaaaaa aaaaaaaaa aa 972

<210> 359

<211> 135

<212> PRT

<213> Homo sapiens

<400> 359

Met	Arg	Ile	Met	Leu	Leu	Phe	Thr	Ala	Ile	Leu	Ala	Phe	Ser	Leu	1	5	10	15
Ala	Gln	Ser	Phe	Gly	Ala	Val	Cys	Lys	Glu	Pro	Gln	Glu	Glu	Val	20	25	30	
Val	Pro	Gly	Gly	Gly	Arg	Ser	Lys	Arg	Asp	Pro	Asp	Leu	Tyr	Gln	35	40	45	
Leu	Leu	Gln	Arg	Leu	Phe	Lys	Ser	His	Ser	Ser	Leu	Glu	Gly	Leu	50	55	60	
Leu	Lys	Ala	Leu	Ser	Gln	Ala	Ser	Thr	Asp	Pro	Lys	Glu	Ser	Thr	65	70	75	
Ser	Pro	Glu	Lys	Arg	Asp	Met	His	Asp	Phe	Phe	Val	Gly	Leu	Met	80	85	90	
Gly	Lys	Arg	Ser	Val	Gln	Pro	Glu	Gly	Lys	Thr	Gly	Pro	Phe	Leu	95	100	105	
Pro	Ser	Val	Arg	Val	Pro	Arg	Pro	Leu	His	Pro	Asn	Gln	Leu	Gly	110	115	120	



Ser Thr Gly Lys Ser Ser Leu Gly Thr Glu Glu Gln Arg Pro Leu  
125 130 135

<210> 360  
<211> 1738  
<212> DNA  
<213> Homo sapiens

<400> 360  
gggcgtctcc ggctgctcct attgagctgt ctgctcgctg tgcccgctgt 50  
gcctgctgtg cccgcgctgt cgcgcgctgt accgcgctgt ctggacgcgg 100  
gagacgcccag cgagctggtg attggagccc tgcggagagc tcaagcgccc 150  
agctctgccc caggagccca ggctgcccag tgagtcccat agttgctgca 200  
ggagtggagc catgagctgc gtccctgggtg gtgtcatccc cttggggctg 250  
ctgttctctg tctgcggatc ccaaggctac ctctcgccca acgtcactct 300  
cttagaggag ctgctcagca aataccagca caacgagtct cactccgggg 350  
tccgcagagc catccccagg gaggacaagg aggagatcct catgtgcac 400  
aacaagcttc ggggccagggt gcagcctcag gcctccaaca tggagtacat 450  
ggtgagcgcc ggctccggcc gcagaggctg gcaccggggg tggggcctgg 500  
gccaccagcc tgtctgttcc ccagccagc tctgttcccc agccagtgcg 550  
tgtgatggct ggctcaggggt ctctctggc aggggaggat ccgggctctg 600  
ttctgttttg ttgtttgtt ttgagacagg gtctcactct gccactgacg 650  
ctggagtgca atggcacaat cgtcatgccc tgaaacctta gactccgggg 700  
gttaagcgat cctgcttcag cctcccaagt agctggaact acaggcatgc 750  
accatggtgc ccagctagat tttaaatatt ttgtggagat gggggctttg 800  
ctacgttgcc caggctggtc ttgaactcct aggtcgaagc aatcctctg 850  
cctcagcctc taaaagtgtc aggattatag gcatgagtca ccctgtctgg 900  
ctctggctct gttcttaaca ttctgcaaaa acaacacacg tgggttccct 950  
gtgcagagcc tgcctcgttg ccttcattgc actcttggtg gctccaactg 1000  
gaacacagct ctacgccttt ccacactgga ggcagagtgg ggaggggccc 1050  
agggctgggc ttgtctgatg ctgatctcag ctgtgccaca cgctagtgc 1100  
accaccctga cttctcctta gcccggtgta gcctcacttt ccacttggag 1150  
agtccttctc gcgctgggtg ccattgactgt gagataagtc gaggctgtga 1200  
agggcccgcc acagactgac ctgcctcccc aacctctagg ctttgctaac 1250  
cgggaaagga gctaacgggtg acagaagaca gccaaaggta accctcccg 1300  
gtgatttgta tgggtgttcc aggtgtggtt gggcgatgct gctacttgac 1350

cccaagctcc agtgtggaac ctctcttctt ggctgggttt ccagaactac 1400  
 agaggaatag accacagtct tccaggggtcc ctctctgtcc accaaccggg 1450  
 agcctccacc ttggccatcc gtcagctatg aatggctttt taaacaaacc 1500  
 cactgtccag cctgggtaac atggtaaagc cccgtctcta caaaaaaacc 1550  
 caagttagcc gggcatggtg gtgcgcacct gtagtccag ctgcagtggg 1600  
 actgaggtgg aggtggaggt ggggggtggg agctgaggaa ggaggatcgc 1650  
 ttgagcctgg gaagtgcagg ctgcagttag ctgagattgc accactgcac 1700  
 tccagcctgg gtgacagagc aagacctgt ctcaaaaa 1738

<210> 361  
 <211> 159  
 <212> PRT  
 <213> Homo sapiens

<400> 361  
 Met Ser Cys Val Leu Gly Gly Val Ile Pro Leu Gly Leu Leu Phe  
 1 5 10 15  
 Leu Val Cys Gly Ser Gln Gly Tyr Leu Leu Pro Asn Val Thr Leu  
 20 25 30  
 Leu Glu Glu Leu Leu Ser Lys Tyr Gln His Asn Glu Ser His Ser  
 35 40 45  
 Arg Val Arg Arg Ala Ile Pro Arg Glu Asp Lys Glu Glu Ile Leu  
 50 55 60  
 Met Leu His Asn Lys Leu Arg Gly Gln Val Gln Pro Gln Ala Ser  
 65 70 75  
 Asn Met Glu Tyr Met Val Ser Ala Gly Ser Gly Arg Arg Gly Trp  
 80 85 90  
 His Arg Gly Trp Gly Leu Gly His Gln Pro Ala Leu Phe Pro Ser  
 95 100 105  
 Gln Leu Cys Ser Pro Ala Ser Ala Cys Asp Gly Trp Leu Arg Val  
 110 115 120  
 Ser Ser Gly Arg Gly Gly Ser Arg Leu Cys Ser Val Leu Phe Val  
 125 130 135  
 Cys Phe Glu Thr Gly Ser His Ser Ala Thr Asp Ala Gly Val Gln  
 140 145 150  
 Trp His Asn Arg His Ala Leu Lys Pro  
 155

<210> 362  
 <211> 422  
 <212> DNA  
 <213> Homo sapiens

<400> 362  
 aaggagaggc caccgggact tcagtgtctc ctccatccca ggagcgcagt 50

ggccactatg gggctcgggc tgccccttgt cctcctcttg accctccttg 100  
gcagctcaca tggaacaggc ccgggtatga ctttgcaact gaagctgaag 150  
gagtcctttc tgacaaatcc ctccatgatg tccagcttcc tggattgct 200  
tgaaagagcgc tgcctcctcc tccatctccc ttcagggacc agcgtcacc 250  
tccaccatgc aagatctcaa caccatgttg tctgcaacac atgacagcca 300  
ttgaagcctg tgtccttctt ggcccgggct tttgggcccgg ggaagcagga 350  
ggcaggcccc gacctgtct ttcagcaggc cccaccctc ctgagtggca 400  
ataaataaaa ttcggtatgc tg 422

<210> 363  
<211> 78  
<212> PRT  
<213> Homo sapiens

<400> 363  
Met Gly Ser Gly Leu Pro Leu Val Leu Leu Leu Thr Leu Leu Gly  
1 5 10 15  
Ser Ser His Gly Thr Gly Pro Gly Met Thr Leu Gln Leu Lys Leu  
20 25 30  
Lys Glu Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe Leu  
35 40 45  
Glu Leu Leu Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly  
50 55 60  
Thr Ser Val Thr Leu His His Ala Arg Ser Gln His His Val Val  
65 70 75  
Cys Asn Thr

<210> 364  
<211> 826  
<212> DNA  
<213> Homo sapiens

<400> 364  
aattgtatct gtgtaatgtt aaaacaaacg aaataaaata gaaggaaaaa 50  
ctttctgagt ttcaaaaaca acagactagt actctaaaga actctttaaa 100  
acaattaact gttaggattg cagttatgat tggatattat ttaattctgt 150  
ttctgatgtg gggttcctcc actgtgttct gtgtgctatt aatatttacc 200  
attgcagaag ctccattcag tgttgaaaat gaatgcttag tggatctgtg 250  
cctcttacgc atatgttaca aattatctgg agttcctaata caatgcagag 300  
ttccccctcc ctccgattgt tctaaataat tgaaagatgt ctgctgtgga 350  
aaaaggcatg tattttaaac tgtatgattc tcaaccatct ttagttggga 400  
aaggctcctg aaagccaatg gaaatacttt ttttttttct tggcactaat 450

caagtgaagt ttaccttttc acttagtagg atgtgttgtt acgctagtaa 500  
aatagaaacc tgtgtttatt ctcaaggatt ttagaacaa cagccatcat 550  
ttttttttat gtgtgtgtt ttgggtgtat tcaataatta tatattttgg 600  
gctatcaaat attacttcat tcaatataaa taacaatagt agaagttgtt 650  
tacttagata tgctttctag ttgcattttc tcagcctatg taagactact 700  
ttgttgtaat agcctttgaa atttacagta ctgtctctct actatcttca 750  
gattacttga ttcaaataaa ccaattatgt ttgtaattga tattaataaa 800  
accagaataa aagttcatat ctaccc 826

<210> 365  
<211> 67  
<212> PRT  
<213> Homo sapiens

<400> 365  
Met Ile Gly Tyr Tyr Leu Ile Leu Phe Leu Met Trp Gly Ser Ser  
1 5 10 15  
Thr Val Phe Cys Val Leu Leu Ile Phe Thr Ile Ala Glu Ala Ser  
20 25 30  
Phe Ser Val Glu Asn Glu Cys Leu Val Asp Leu Cys Leu Leu Arg  
35 40 45  
Ile Cys Tyr Lys Leu Ser Gly Val Pro Asn Gln Cys Arg Val Pro  
50 55 60  
Leu Pro Ser Asp Cys Ser Lys  
65

<210> 366  
<211> 2475  
<212> DNA  
<213> Homo sapiens

<400> 366  
gaggatttgc cacagcagcg gatagagcag gagagcacca cggagccct 50  
tgagacatcc ttgagaagag ccacagcata agagactgcc ctgcttggtg 100  
ttttgcagga tgatggtggc ccttcgagga gcttctgcat tgctgtttct 150  
gttccttgca gcttttctgc ccccgccgca gtgtaccag gaccagcca 200  
tgggtgatta catctaccag cgctttcgag tcttggagca agggctggaa 250  
aatgtatccc aagcaacgag ggcatacatt caagaattcc aagagttctc 300  
aaaaatata tctgtcatgc tgggaagatg tcagacctac acaagtgaagt 350  
acaagagtgc agtgggtaac ttggcaactga gagttgaacg tgcccaacgg 400  
gagattgact acatacaata ccttcgagag gctgacgagt gcatogtata 450  
agaggacaag acactggcag aaatgttgct ccaagaagct gaagaagaga 500

aaaagatccg gactctgctg aatgcaagct gtgacaacat gctgatgggc 550  
 ataaagtctt tgaataatag gaagaagatg atggacacac atggctcttg 600  
 gatgaagat gctgtctata actctccaaa ggtgtactta ttaattggat 650  
 ccagaacaa cactgttttg gaatttgcaa acatacgggc attcatggag 700  
 gataaacca agccagctco ccggaagcaa atcctaacac ttctctggca 750  
 gggaacaggc caagtgatct acaaagggtt tctatttttt cataaccaag 800  
 caacttctaa tgagataatc aatatatacc tgcagaagag gactgtggaa 850  
 gatcgaatgc tgctcccagg aggggttaggc cgagcattgg ttaccagca 900  
 ctccccctca acttacattg acctggctgt ggatgagcat gggtctggg 950  
 ccatccactc tgggccaggc acccatagcc atttggttct cacaaagatt 1000  
 gagccgggca cactgggagt ggagcattca tgggataccc catgcagaag 1050  
 ccaggatgct gaagcctcat tcctcttggt tggggttctc tatgtgtct 1100  
 acagtactgg gggccagggc cctcatcgca tcacctgcat ctatgatcca 1150  
 ctgggcacta tcagttagga ggacttgccc aactgttct tcccaagag 1200  
 accaagaagt cactccatga tcattacaa cccagagat aagcagctct 1250  
 atgcctggaa tgaaggaaac cagatcattt acaactcca gacaaagaga 1300  
 aagctgcctc tgaagtaatg cattacagct gtgagaaaga gcactgtggc 1350  
 ttggcagct gttctacagg acagttaggc tatagccct tcacaatata 1400  
 gtatccctct aatcacacac aggaagagtg tgtagaagtg gaaatacgta 1450  
 tgctccttt cccaaatgtc actgccttag gtatcttcca agagcttaga 1500  
 tgagagcata tcatcaggaa agtttcaaca atgtccatta ctccccaaa 1550  
 cctcctggct ctcaaggatg accacattct gatacagcct acttcaagcc 1600  
 ttttgtttta ctgctcccca gcatttactg taactctgcc atcttccctc 1650  
 ccacaattag agttgtatgc cagccctcaa tttccaccac tggtttttct 1700  
 ctccccctgc ctttgetgaa gctcttcct ctttttcaaa tgtctattga 1750  
 tattctccca ttttcaactgc ccaactaaaa tactattaat atttctttct 1800  
 tttcttttct tttttttgag acaaggctct actatgttgc ccaggctggg 1850  
 ctcaaaactc agagctcaag agatcctcct gcctcagcct cctaagtacc 1900  
 tgggattaca ggcattgtgc accacacctg gcttaaaata ctatttttta 1950  
 ttgaggttta acctctattt cccttagccc tgccttcca ctaagcttgg 2000  
 tagatgtaat aataaagtga aaatattaac atttgaatat cgctttccag 2050  
 gtgtggagtg tttgcacatc attgaattct cgtttcacct ttgtgaaaca 2100

tgcacaagtc ttacagctg tcattctaga gtttaggtga gtaacacaat 2150  
 tacaaagtga aagatacagc tagaaaatac tacaaatccc atagtttttc 2200  
 cattgcccaa ggaagcatca aatacgatg tttgttcacc tactottata 2250  
 gtcaatgcgt tcacgttttc agcctaaaaa taatagtctg tccctttagc 2300  
 cagttttcat gtctgcacaa gacctttcaa taggcctttc aatgataat 2350  
 tctocagaa aaccagtcta agggtagga ccccaactct agcctcctct 2400  
 tgtcttgctg tctctggtt ctctctttct gctttaaatt caataaaagt 2450  
 gacactgagc aaaaaaaaaa aaaaa 2475

<210> 367  
 <211> 402  
 <212> PRT  
 <213> Homo sapiens

<400> 367  
 Met Met Val Ala Leu Arg Gly Ala Ser Ala Leu Leu Val Leu Phe  
 1 5 10 15  
 Leu Ala Ala Phe Leu Pro Pro Pro Gln Cys Thr Gln Asp Pro Ala  
 20 25 30  
 Met Val His Tyr Ile Tyr Gln Arg Phe Arg Val Leu Glu Gln Gly  
 35 40 45  
 Leu Glu Lys Cys Thr Gln Ala Thr Arg Ala Tyr Ile Gln Glu Phe  
 50 55 60  
 Gln Glu Phe Ser Lys Asn Ile Ser Val Met Leu Gly Arg Cys Gln  
 65 70 75  
 Thr Tyr Thr Ser Glu Tyr Lys Ser Ala Val Gly Asn Leu Ala Leu  
 80 85 90  
 Arg Val Glu Arg Ala Gln Arg Glu Ile Asp Tyr Ile Gln Tyr Leu  
 95 100 105  
 Arg Glu Ala Asp Glu Cys Ile Val Ser Glu Asp Lys Thr Leu Ala  
 110 115 120  
 Glu Met Leu Leu Gln Glu Ala Glu Glu Lys Lys Ile Arg Thr  
 125 130 135  
 Leu Leu Asn Ala Ser Cys Asp Asn Met Leu Met Gly Ile Lys Ser  
 140 145 150  
 Leu Lys Ile Val Lys Lys Met Met Asp Thr His Gly Ser Trp Met  
 155 160 165  
 Lys Asp Ala Val Tyr Asn Ser Pro Lys Val Tyr Leu Leu Ile Gly  
 170 175 180  
 Ser Arg Asn Asn Thr Val Trp Glu Phe Ala Asn Ile Arg Ala Phe  
 185 190 195  
 Met Glu Asp Asn Thr Lys Pro Ala Pro Arg Lys Gln Ile Leu Thr  
 200 205 210

Leu Ser Trp Gln Gly Thr Gly Gln Val Ile Tyr Lys Gly Phe Leu  
 215 220  
 Phe Phe His Asn Gln Ala Thr Ser Asn Glu Ile Ile Lys Tyr Asn  
 230 235 240  
 Leu Gln Lys Arg Thr Val Glu Asp Arg Met Leu Leu Pro Gly Gly  
 245 250 255  
 Val Gly Arg Ala Leu Val Tyr Gln His Ser Pro Ser Thr Tyr  
 260 265 270  
 Asp Leu Ala Val Asp Glu His Gly Leu Trp Ala Ile His Ser Gly  
 275 280 285  
 Pro Gly Thr His Ser His Leu Val Leu Thr Lys Ile Glu Pro Gly  
 290 295 300  
 Thr Leu Gly Val Glu His Ser Trp Asp Thr Pro Cys Arg Ser Gln  
 305 310 315  
 Asp Ala Glu Ala Ser Phe Leu Leu Cys Gly Val Leu Tyr Val Val  
 320 325 330  
 Tyr Ser Thr Gly Gly Gln Gly Pro His Arg Ile Thr Cys Ile Tyr  
 335 340 345  
 Asp Pro Leu Gly Thr Ile Ser Glu Glu Asp Leu Pro Asn Leu Phe  
 350 355 360  
 Phe Pro Lys Arg Pro Arg Ser His Ser Met Ile His Tyr Asn Pro  
 365 370 375  
 Arg Asp Lys Gln Leu Tyr Ala Trp Asn Glu Gly Asn Gln Ile Ile  
 380 385 390  
 Tyr Lys Leu Gln Thr Lys Arg Lys Leu Pro Leu Lys  
 395 400

<210> 368  
 <211> 2281  
 <212> DNA  
 <213> Homo sapiens

<400> 368  
 gggcgccgc gtactcacta gctgaggtgg cagtgggtcc accaacaatgg 50  
 agctctcgca gatgtcggag ctcatggggc tgtcgggtgtt gcttggggtg 100  
 ctggccctga tggcgacggc ggcggttagcg cgggggtggc tgcgcgcggg 150  
 ggaggagagg agcggccggc ccgcctgcc aaaaagcaaat ggatttcac 200  
 ctgacaaatc ttcgggatcc aagaagcaga aacaatatca gcggattcgg 250  
 aaggagaagc ctcaacaaca caacttcacc caccgcctcc tggctgcagc 300  
 tctgaagagc cacagcggga acatatcttg catggacttt agcagcaatg 350  
 gcaaatacct ggctacctgt gcagatgac gcaccatcgg catctggagc 400  
 accaaggact tcctgcagcg agagcaccgc agcatgagag ccaacgtgga 450

gctggaccac gccacccctgg tgcgcttcag ccctgactgc agagccttca 500  
 tcgtctggct ggccaacggg gacaccctcc gtgtcttcaa gatgaccaag 550  
 cgggaggatg ggggctacac cttcacagcc accccagagg acttccctaa 600  
 aaagcacaag gcgcctgtca tcgacattgg cattgtcaac acagggaagt 650  
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 <211> 447  
 <212> PRT  
 <213> Homo sapiens

<400> 369  
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 Lys Ala Asn Gly Phe Pro Pro Asp Lys Ser Ser Gly Ser Lys Lys  
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 Gln Lys Gln Tyr Gln Arg Ile Arg Lys Glu Lys Pro Gln Gln His  
 65 70 75  
 Asn Phe Thr His Arg Leu Leu Ala Ala Leu Lys Ser His Ser  
 80 85 90  
 Gly Asn Ile Ser Cys Met Asp Phe Ser Ser Asn Gly Lys Tyr Leu  
 95 100 105  
 Ala Thr Cys Ala Asp Asp Arg Thr Ile Arg Ile Trp Ser Thr Lys  
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 125 130 135  
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 Phe Ile Val Trp Leu Ala Asn Gly Asp Thr Leu Arg Val Phe Lys  
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 Met Thr Lys Arg Glu Asp Gly Gly Tyr Thr Phe Thr Ala Thr Pro  
 170 175 180  
 Glu Asp Phe Pro Lys Lys His Lys Ala Pro Val Ile Asp Ile Gly  
 185 190 195  
 Ile Ala Asn Thr Gly Lys Phe Ile Met Thr Ala Ser Ser Asp Thr  
 200 205 210  
 Thr Val Leu Ile Trp Ser Leu Lys Gly Gln Val Leu Ser Thr Ile  
 215 220 225  
 Asn Thr Asn Gln Met Asn Asn Thr His Ala Ala Val Ser Pro Cys  
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Gly	Arg	Phe	Val	Ala	Ser	Cys	Gly	Phe	Thr	Pro	Asp	Val	Lys	Val	245	250	255
Trp	Glu	Val	Cys	Phe	Gly	Lys	Lys	Gly	Glu	Phe	Gln	Glu	Val	Val	260	265	270
Arg	Ala	Phe	Glu	Leu	Lys	Gly	His	Ser	Ala	Ala	Val	His	Ser	Phe	275	280	285
Ala	Phe	Ser	Asn	Asp	Ser	Arg	Arg	Met	Ala	Ser	Val	Ser	Lys	Asp	290	295	300
Gly	Thr	Trp	Lys	Leu	Trp	Asp	Thr	Asp	Val	Glu	Tyr	Lys	Lys	Lys	305	310	315
Gln	Asp	Pro	Tyr	Leu	Leu	Lys	Thr	Gly	Arg	Phe	Glu	Glu	Ala	Ala	320	325	330
Gly	Ala	Ala	Pro	Cys	Arg	Leu	Ala	Leu	Ser	Pro	Asn	Ala	Gln	Val	335	340	345
Leu	Ala	Leu	Ala	Ser	Gly	Ser	Ser	Ile	His	Leu	Tyr	Asn	Thr	Arg	350	355	360
Arg	Gly	Glu	Lys	Glu	Glu	Cys	Phe	Glu	Arg	Val	His	Gly	Glu	Cys	365	370	375
Ile	Ala	Asn	Leu	Ser	Phe	Asp	Ile	Thr	Gly	Arg	Phe	Leu	Ala	Ser	380	385	390
Cys	Gly	Asp	Arg	Ala	Val	Arg	Leu	Phe	His	Asn	Thr	Pro	Gly	His	395	400	405
Arg	Ala	Met	Val	Glu	Glu	Met	Gln	Gly	His	Leu	Lys	Arg	Ala	Ser	410	415	420
Asn	Glu	Ser	Thr	Arg	Gln	Arg	Leu	Gln	Gln	Gln	Leu	Thr	Gln	Ala	425	430	435
Gln	Glu	Thr	Leu	Lys	Ser	Leu	Gly	Ala	Leu	Lys	Lys				440	445	

<210> 370

<211> 1415

<212> DNA

<213> Homo sapiens

<400> 370

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<210> 371  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 371  
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 35 40 45  
 Gly Leu Arg Met Cys Thr Pro Leu Gly Arg Glu Gly Glu Glu Cys  
 50 55 60  
 His Pro Gly Ser His Lys Val Pro Phe Phe Arg Lys Arg Lys His  
 65 70 75

His Thr Cys Pro Cys Leu Pro Asn Leu Leu Cys Ser Arg Phe Pro  
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Asp Gly Arg Tyr Arg Cys Ser Met Asp Leu Lys Asn Ile Asn Phe  
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<210> 372

<211> 1281

<212> DNA

<213> Homo sapiens

<400> 372

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 <211> 229  
 <212> PRT  
 <213> Homo sapiens

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 35 40 45  
 Leu Glu Tyr Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu  
 50 55 60  
 Pro Arg Thr Phe Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala  
 65 70 75  
 Val Ile Met Ala Val Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu  
 80 85 90  
 Glu Ala Ala Asp Leu Ser Ser Leu Lys Ser Met Leu Asp Gln Leu  
 95 100 105  
 Gly Val Pro Leu Tyr Ala Val Val Lys Glu His Ile Arg Thr Glu  
 110 115 120  
 Val Lys Asp Phe Gln Pro Tyr Phe Lys Gly Glu Ile Phe Leu Asp  
 125 130 135  
 Glu Lys Lys Lys Phe Tyr Gly Pro Gln Arg Arg Lys Met Met Phe  
 140 145 150  
 Met Gly Phe Ile Arg Leu Gly Val Trp Tyr Asn Phe Phe Arg Ala  
 155 160 165  
 Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly Glu Gly Phe Ile  
 170 175 180  
 Leu Gly Gly Val Phe Val Val Gly Ser Gly Lys Gln Gly Ile Leu  
 185 190 195  
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 200 205 210  
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<210> 374  
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 <212> DNA  
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<210> 375  
<211> 123  
<212> PRT  
<213> Homo sapiens

<400> 375  
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Thr Ser Ala Asn Glu Asn Ser Thr Val Leu Pro Ser Ser Thr Ser  
35 40 45  
Ser Ser Ser Asp Gly Asn Leu Arg Pro Glu Ala Ile Thr Ala Ile  
50 55 60  
Ile Val Val Phe Ser Leu Leu Ala Ala Leu Leu Ala Val Gly  
65 70 75  
Leu Ala Leu Leu Val Arg Lys Leu Arg Glu Lys Arg Gln Thr Glu  
80 85 90  
Gly Thr Tyr Arg Pro Ser Ser Glu Glu Gln Phe Ser His Ala Ala  
95 100 105  
Glu Ala Arg Ala Pro Gln Asp Ser Lys Glu Thr Val Gln Gly Cys  
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<210> 376  
<211> 713  
<212> DNA  
<213> Homo sapiens

<400> 376  
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<210> 377  
<211> 90  
<212> PRT  
<213> Homo sapiens

<400> 377  
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35 40 45  
Ser Leu Glu Asp Ser Val Thr Pro Thr Lys Ala Val Lys Thr Thr  
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<210> 378  
<211> 3265  
<212> DNA  
<213> Homo sapiens

<400> 378  
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<210> 379  
 <211> 919  
 <212> PRT  
 <213> Homo sapiens

<400> 379

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				20					25						
Phe	Glu	Asp	Ile	Val	Ile	Val	Ile	Asp	Pro	Ser	Val	Pro	Glu	Asp	45
				35					40						
Glu	Lys	Ile	Ile	Glu	Gln	Ile	Glu	Asp	Met	Val	Thr	Thr	Ala	Ser	60
				50					55						
Thr	Tyr	Leu	Phe	Glu	Ala	Thr	Glu	Lys	Arg	Phe	Phe	Phe	Lys	Asn	75
				65					70						
Val	Ser	Ile	Leu	Ile	Pro	Glu	Asn	Trp	Lys	Glu	Asn	Pro	Gln	Tyr	90
				80					85						
Lys	Arg	Pro	Lys	His	Glu	Asn	His	Lys	His	Ala	Asp	Val	Ile	Val	105
				95					100						
Ala	Pro	Pro	Thr	Leu	Pro	Gly	Arg	Asp	Glu	Pro	Tyr	Thr	Lys	Gln	120
				110					115						
Phe	Thr	Glu	Cys	Gly	Glu	Lys	Gly	Glu	Tyr	Ile	His	Phe	Thr	Pro	135
				125					130						
Asp	Leu	Leu	Leu	Gly	Lys	Lys	Gln	Asn	Glu	Tyr	Gly	Pro	Pro	Gly	150
				140					145						
Lys	Leu	Phe	Val	His	Glu	Trp	Ala	His	Leu	Arg	Trp	Gly	Val	Phe	165
				155					160						
Asp	Glu	Tyr	Asn	Glu	Asp	Gln	Pro	Phe	Tyr	Arg	Ala	Lys	Ser	Lys	180
				170					175						
Lys	Ile	Glu	Ala	Thr	Arg	Cys	Ser	Ala	Gly	Ile	Ser	Gly	Arg	Asn	195
				185					190						
Arg	Val	Tyr	Lys	Cys	Gln	Gly	Gly	Ser	Cys	Leu	Ser	Arg	Ala	Cys	210
				200					205						
Arg	Ile	Asp	Ser	Thr	Thr	Lys	Leu	Tyr	Gly	Lys	Asp	Cys	Gln	Phe	225
				215					220						
Phe	Pro	Asp	Lys	Val	Gln	Thr	Glu	Lys	Ala	Ser	Ile	Met	Phe	Met	240
				230					235						
Gln	Ser	Ile	Asp	Ser	Val	Val	Glu	Phe	Cys	Asn	Glu	Lys	Thr	His	255
				245					250						
Asn	Gln	Glu	Ala	Pro	Ser	Leu	Gln	Asn	Ile	Lys	Cys	Asn	Phe	Arg	270
				260					265						
Ser	Thr	Trp	Glu	Val	Ile	Ser	Asn	Ser	Glu	Asp	Phe	Lys	Asn	Thr	

275	280	285
Ile Pro Met Val Thr Pro Pro Pro Pro Pro Val Phe Ser Leu Leu		
290	295	300
Lys Ile Ser Gln Arg Ile Val Cys Leu Val Leu Asp Lys Ser Gly		
305	310	315
Ser Met Gly Gly Lys Asp Arg Leu Asn Arg Met Asn Gln Ala Ala		
320	325	330
Lys His Phe Leu Leu Gln Thr Val Glu Asn Gly Ser Trp Val Gly		
335	340	345
Met Val His Phe Asp Ser Thr Ala Thr Ile Val Asn Lys Leu Ile		
350	355	360
Gln Ile Lys Ser Ser Asp Glu Arg Asn Thr Leu Met Ala Gly Leu		
365	370	375
Pro Thr Tyr Pro Leu Gly Gly Thr Ser Ile Cys Ser Gly Ile Lys		
380	385	390
Tyr Ala Phe Gln Val Ile Gly Glu Leu His Ser Gln Leu Asp Gly		
395	400	405
Ser Glu Val Leu Leu Leu Thr Asp Gly Glu Asp Asn Thr Ala Ser		
410	415	420
Ser Cys Ile Asp Glu Val Lys Gln Ser Gly Ala Ile Val His Phe		
425	430	435
Ile Ala Leu Gly Arg Ala Ala Asp Glu Ala Val Ile Glu Met Ser		
440	445	450
Lys Ile Thr Gly Gly Ser His Phe Tyr Val Ser Asp Glu Ala Gln		
455	460	465
Asn Asn Gly Leu Ile Asp Ala Phe Gly Ala Leu Thr Ser Gly Asn		
470	475	480
Thr Asp Leu Ser Gln Lys Ser Leu Gln Leu Glu Ser Lys Gly Leu		
485	490	495
Thr Leu Asn Ser Asn Ala Trp Met Asn Asp Thr Val Ile Ile Asn		
500	505	510
Ser Thr Val Gly Lys Asp Thr Phe Phe Leu Ile Thr Trp Asn Ser		
515	520	525
Leu Pro Pro Ser Ile Ser Leu Trp Asp Pro Ser Gly Thr Ile Met		
530	535	540
Glu Asn Phe Thr Val Asp Ala Thr Ser Lys Met Ala Tyr Leu Ser		
545	550	555
Ile Pro Gly Thr Ala Lys Val Gly Thr Trp Ala Tyr Asn Leu Gln		
560	565	570
Ala Lys Ala Asn Pro Glu Thr Leu Thr Ile Thr Val Thr Ser Arg		
575	580	585
Ala Ala Asn Ser Ser Val Pro Pro Ile Thr Val Asn Ala Lys Met		

	590		595		600
Asn Lys Asp Val	Asn Ser Phe Pro Ser	Pro Met Ile Val Tyr Ala			
	605		610		615
Glu Ile Leu Gln Gly	Tyr Val Pro Val	Leu Gly Ala Asn Val Thr			
	620		625		630
Ala Phe Ile Glu Ser	Gln Asn Gly His Thr	Glu Val Leu Glu Leu			
	635		640		645
Leu Asp Asn Gly	Ala Gly Ala Asp Ser	Phe Lys Asn Asp Gly Val			
	650		655		660
Tyr Ser Arg Tyr	Phe Thr Ala Tyr Thr	Glu Asn Gly Arg Tyr Ser			
	665		670		675
Leu Lys Val Arg	Ala His Gly Gly Ala	Asn Thr Ala Arg Leu Lys			
	680		685		690
Leu Arg Pro Pro	Leu Asn Arg Ala Ala	Tyr Ile Pro Gly Trp Val			
	695		700		705
Val Asn Gly Glu	Ile Glu Ala Asn Pro	Pro Arg Pro Glu Ile Asp			
	710		715		720
Glu Asp Thr Gln	Thr Thr Leu Glu Asp	Phe Ser Arg Thr Ala Ser			
	725		730		735
Gly Gly Ala Phe	Val Val Ser Gln Val	Pro Ser Leu Pro Leu Pro			
	740		745		750
Asp Gln Tyr Pro	Pro Ser Gln Ile Thr	Asp Leu Asp Ala Thr Val			
	755		760		765
His Glu Asp Lys	Ile Ile Leu Thr Trp	Thr Ala Pro Gly Asp Asn			
	770		775		780
Phe Asp Val Gly	Lys Val Gln Arg Tyr	Ile Ile Arg Ile Ser Ala			
	785		790		795
Ser Ile Leu Asp	Leu Arg Asp Ser Phe	Asp Asp Ala Leu Gln Val			
	800		805		810
Asn Thr Thr Asp	Leu Ser Pro Lys Glu	Ala Asn Ser Lys Glu Ser			
	815		820		825
Phe Ala Phe Lys	Pro Glu Asn Ile Ser	Glu Glu Asn Ala Thr His			
	830		835		840
Ile Phe Ile Ala	Ile Lys Ser Ile Asp	Lys Ser Asn Leu Thr Ser			
	845		850		855
Lys Val Ser Asn	Ile Ala Gln Val Thr	Leu Phe Ile Pro Gln Ala			
	860		865		870
Asn Pro Asp Asp	Ile Asp Pro Thr Pro	Thr Pro Thr Pro Thr Pro			
	875		880		885
Thr Pro Asp Lys	Ser His Asn Ser Gly	Val Asn Ile Ser Thr Leu			
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Val Leu Ser Val	Ile Gly Ser Val Val	Ile Val Asn Phe Ile Leu			

Ser Thr Thr Ile

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 <211> 3877  
 <212> DNA  
 <213> Homo sapiens

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 cccagttat gccaggattt actagagagt gtcaactcaa ccagcaagcg 250  
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 <212> PRT  
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 Met Leu Ala Cys Thr Pro Lys Gly Asp Glu Gln Leu Ala Leu  
 35 40 45  
 Pro Arg Ala Asn Ser Pro Thr Gly Lys Glu Gly Tyr Gln Ala Val  
 50 55 60  
 Leu Gln Glu Trp Glu Glu Gln His Arg Asn Tyr Val Ser Ser Leu  
 65 70 75  
 Lys Arg Gln Ile Ala Gln Leu Lys Glu Glu Leu Gln Glu Arg Ser  
 80 85 90

Glu	Gln	Leu	Arg	Asn	Gly	Gln	Tyr	Gln	Ala	Ser	Asp	Ala	Ala	Gly	
				95					100					105	
Leu	Gly	Leu	Asp	Arg	Ser	Pro	Pro	Glu	Lys	Thr	Gln	Ala	Asp	Leu	
				110					115					120	
Leu	Ala	Phe	Leu	His	Ser	Gln	Val	Asp	Lys	Ala	Glu	Val	Asn	Ala	
				125					130					135	
Gly	Val	Lys	Leu	Ala	Thr	Glu	Tyr	Ala	Ala	Val	Pro	Phe	Asp	Ser	
				140					145					150	
Phe	Thr	Leu	Gln	Lys	Val	Tyr	Gln	Leu	Glu	Thr	Gly	Leu	Thr	Arg	
				155					160					165	
His	Pro	Glu	Glu	Lys	Pro	Val	Arg	Lys	Asp	Lys	Arg	Asp	Glu	Leu	
				170					175					180	
Val	Glu	Ala	Ile	Glu	Ser	Ala	Leu	Glu	Thr	Leu	Asn	Asn	Pro	Ala	
				185					190					195	
Glu	Asn	Ser	Pro	Asn	His	Arg	Pro	Tyr	Thr	Ala	Ser	Asp	Phe	Ile	
				200					205					210	
Glu	Gly	Ile	Tyr	Arg	Thr	Glu	Arg	Asp	Lys	Gly	Thr	Leu	Tyr	Glu	
				215					220					225	
Leu	Thr	Phe	Lys	Gly	Asp	His	Lys	His	Glu	Phe	Lys	Arg	Leu	Ile	
				230					235					240	
Leu	Phe	Arg	Pro	Phe	Ser	Pro	Ile	Met	Lys	Val	Lys	Asn	Glu	Lys	
				245					250					255	
Leu	Asn	Met	Ala	Asn	Thr	Leu	Ile	Asn	Val	Ile	Val	Pro	Leu	Ala	
				260					265					270	
Lys	Arg	Val	Asp	Lys	Phe	Arg	Gln	Phe	Met	Gln	Asn	Phe	Arg	Glu	
				275					280					285	
Met	Cys	Ile	Glu	Gln	Asp	Gly	Arg	Val	His	Leu	Thr	Val	Val	Tyr	
				290					295					300	
Phe	Gly	Lys	Glu	Glu	Ile	Asn	Glu	Val	Lys	Gly	Ile	Leu	Glu	Asn	
				305					310					315	
Thr	Ser	Lys	Ala	Ala	Asn	Phe	Arg	Asn	Phe	Thr	Phe	Ile	Gln	Leu	
				320					325					330	
Asn	Gly	Glu	Phe	Ser	Arg	Gly	Lys	Gly	Leu	Asp	Val	Gly	Ala	Arg	
				335					340					345	
Phe	Trp	Lys	Gly	Ser	Asn	Val	Leu	Leu	Phe	Phe	Cys	Asp	Val	Asp	
				350					355					360	
Ile	Tyr	Phe	Thr	Ser	Glu	Phe	Leu	Asn	Thr	Cys	Arg	Leu	Asn	Thr	
				365					370					375	
Gln	Pro	Gly	Lys	Lys	Val	Phe	Tyr	Pro	Val	Leu	Phe	Ser	Gln	Tyr	
				380					385					390	
Asn	Pro	Gly	Ile	Ile	Tyr	Gly	His	His	Asp	Ala	Val	Pro	Pro	Leu	
				395					400					405	



Glu Gln Gln Leu Val Ile Lys Lys Glu Thr Gly Phe Trp Arg Asp  
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 Phe Gly Phe Gly Met Thr Cys Gln Tyr Arg Ser Asp Phe Ile Asn  
 425 430 435  
 Ile Gly Gly Phe Asp Leu Asp Ile Lys Gly Trp Gly Gly Glu Asp  
 440 445 450  
 Val His Leu Tyr Arg Lys Tyr Leu His Ser Asn Leu Ile Val Val  
 455 460 465  
 Arg Thr Pro Val Arg Gly Leu Phe His Leu Trp His Glu Lys Arg  
 470 475 480  
 Cys Met Asp Glu Leu Thr Pro Glu Gln Tyr Lys Met Cys Met Gln  
 485 490 495  
 Ser Lys Ala Met Asn Glu Ala Ser His Gly Gln Leu Gly Met Leu  
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 Val Phe Arg His Glu Ile Glu Ala His Leu Arg Lys Gln Lys Gln  
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 Lys Thr Ser Ser Lys Lys Thr  
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<210> 386

<211> 1346

<212> DNA

<213> Homo sapiens

<400> 386

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ctcttcaaa cgtggtagc tttctccatg agaaaagttc ccaacagaga 200

agcaacagaa atttccatg tctactttg caatgtaacc cagaggggat 250

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gttgaggtgc aatcagccat aagaatgaac aagaaccgga tcaacaatgc 350

cttctttcta aatgaccaa ctctggaatt tttaaaaatc cttctcacac 400

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gatgagaggc tcaccctctc ctgaagggct gttgtttctg ttcctcaaga 700

aattaaacat ttgtttctgt gtgactgctg agcatcctga aataccaaga 750

gcagatcata tattttgttt caccattctt cttttgtaat aaattttgaa 800

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tggaattact catatacagg gtggaatttt atcctgttat cacaccaaca 1200

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<210> 387

<211> 212

<212> PRT

<213> Homo sapiens

<400> 387

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Ile	Arg	Thr	Ala	Leu	Gly	Asp	Lys	Ala	Tyr	Ala	Trp	Asp	Thr	Asn	35	40	45	
Glu	Glu	Tyr	Leu	Phe	Lys	Ala	Met	Val	Ala	Phe	Ser	Met	Arg	Lys	50	55	60	
Val	Pro	Asn	Arg	Glu	Ala	Thr	Glu	Ile	Ser	His	Val	Leu	Leu	Cys	65	70	75	
Asn	Val	Thr	Gln	Arg	Val	Ser	Phe	Trp	Phe	Val	Val	Thr	Asp	Pro	80	85	90	
Ser	Lys	Asn	His	Thr	Leu	Pro	Ala	Val	Glu	Val	Gln	Ser	Ala	Ile	95	100	105	
Arg	Met	Asn	Lys	Asn	Arg	Ile	Asn	Asn	Ala	Phe	Phe	Leu	Asn	Asp	110	115	120	
Gln	Thr	Leu	Glu	Phe	Leu	Lys	Ile	Pro	Ser	Thr	Leu	Ala	Pro	Pro	125	130	135	
Met	Asp	Pro	Ser	Val	Pro	Ile	Trp	Ile	Ile	Ile	Phe	Gly	Val	Ile	140	145	150	
Phe	Cys	Ile	Ile	Ile	Val	Ala	Ile	Ala	Leu	Leu	Ile	Leu	Ser	Gly	155	160	165	
Ile	Trp	Gln	Arg	Arg	Arg	Lys	Asn	Lys	Glu	Pro	Ser	Glu	Val	Asp	170	175	180	
Asp	Ala	Glu	Asp	Lys	Cys	Glu	Asn	Met	Ile	Thr	Ile	Glu	Asn	Gly	185	190	195	
Ile	Pro	Ser	Asp	Pro	Leu	Asp	Met	Lys	Gly	Gly	Ile	Leu	Met	Met	200	205	210	
Pro	Ser																	

<210> 388

<211> 1371

<212> DNA

<213> Homo sapiens

<400> 388

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 gaacaagaac cctagtattt cttgaagtta atggaaactt ttctttggct 850  
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<210> 389

<211> 215

<212> PRT

<213> Homo sapiens

<400> 389

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Ile	Gln	Leu	Thr	Ala	Leu	Trp	Pro	Ile	Ala	Ala	Val	Glu	Ile	Tyr	20	25	30
Thr	Ser	Arg	Val	Leu	Glu	Ala	Val	Asn	Gly	Thr	Asp	Ala	Arg	Leu	35	40	45
Lys	Cys	Thr	Phe	Ser	Ser	Phe	Ala	Pro	Val	Gly	Asp	Ala	Leu	Thr	50	55	60
Val	Thr	Trp	Asn	Phe	Arg	Pro	Leu	Asp	Gly	Gly	Pro	Glu	Gln	Phe	65	70	75
Val	Phe	Tyr	Tyr	His	Ile	Asp	Pro	Phe	Gln	Pro	Met	Ser	Gly	Arg	80	85	90
Phe	Lys	Asp	Arg	Val	Ser	Trp	Asp	Gly	Asn	Pro	Glu	Arg	Tyr	Asp	95	100	105
Ala	Ser	Ile	Leu	Leu	Trp	Lys	Leu	Gln	Phe	Asp	Asp	Asn	Gly	Thr	110	115	120
Tyr	Thr	Cys	Gln	Val	Lys	Asn	Pro	Pro	Asp	Val	Asp	Gly	Val	Ile	125	130	135
Gly	Glu	Ile	Arg	Leu	Ser	Val	Val	His	Thr	Val	Arg	Phe	Ser	Glu	140	145	150
Ile	His	Phe	Leu	Ala	Leu	Ala	Ile	Gly	Ser	Ala	Cys	Ala	Leu	Met	155	160	165
Ile	Ile	Ile	Val	Ile	Val	Val	Val	Leu	Phe	Gln	His	Tyr	Arg	Lys	170	175	180
Lys	Arg	Trp	Ala	Glu	Arg	Ala	His	Lys	Val	Val	Glu	Ile	Lys	Ser	185	190	195
Lys	Glu	Glu	Glu	Arg	Leu	Asn	Gln	Glu	Lys	Lys	Val	Ser	Val	Tyr	200	205	210
Leu	Glu	Asp	Thr	Asp											215		

<210> 390

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 390

ccgaggccat ctagaggcca gagc 24

<210> 391

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

acaggcagag ccaatggcca gagc 24

<210> 392  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 392  
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<210> 393  
 <211> 471  
 <212> DNA  
 <213> Homo sapiens

<400> 393  
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 atccgacaac agctgctcca gctgacacgt atccagctac tggctctgct 150  
 gatgatgaag cccctgatgc tgaaccact gctgctgcaa ccaactgcgac 200  
 cactgctgct cctaccactg caaccaccgc tgctcttacc actgctcgta 250  
 aagacattcc agttttacc aaatgggttg gggatctccc gaatggtaga 300  
 gtgtgtccct gagatggaat cagcttgagt cttctgcaat tggtcacaac 350  
 tattcatgct tccgtgtgatt tcatccaact acttacottg cctacgatat 400  
 cccctttatc totaatcagt ttattttctt tcaataaaaa aataactatg 450  
 agcaacataa aaaaaaaaaa a 471

<210> 394  
 <211> 90  
 <212> PRT  
 <213> Homo sapiens

<400> 394  
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 Leu Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr  
 20 25 30  
 Tyr Pro Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu  
 35 40 45  
 Thr Thr Ala Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr  
 50 55 60  
 Ala Thr Thr Ala Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val  
 65 70 75  
 Leu Pro Lys Trp Val Gly Asp Leu Pro Asn Gly Arg Val Cys Pro  
 80 85 90

<210> 395  
 <211> 25

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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 395
gctccctgat cttcatgtca ccacc 25

<210> 396
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 396
cagggacaca ctctaccatt cgggag 26

<210> 397
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 397
ccatotttct ggtctctgcc cagaatccga caacagctgc tc 42

<210> 398
<211> 907
<212> DNA
<213> Homo sapiens

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gggcaggacc ccatagggga atgctacctc ctgcccttcc acctgccctg 150
gtgttcacgg tggcctggtc cctccttgcc gagagagtgt cctgggtcag 200
ggacgcagag gacgctcaca gactccagcc ctttgttacc gagaggacac 250
ttggcaaggt ccagcgatgg tccggagtcc acacacagac tggcggcagg 300
gcaggagggg gacagttctg ttgtgcttgg ttggacagta agagggtctt 350
ggccagtcca ggggtggggg cggcaaaactc cataaagaac cagagggtct 400
gggccccgpc cacagagtca tctgcccagc tctctgctg ctggccagtg 450
ggagtggcac gagtggggc tttgtgccag taaaaccaca ggctggattt 500
gcctgcgggc catggtccct gtctagggca gcaattctca accttcttgc 550
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agcaattaaa actgagaaat gggccgggca cggtggtcga cgcctgtaat 650

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cccagcactt tgggagggcg aggcgggtgg atcacctgag atcaggagtt 700  
 caagaccagc ctggccaaca tggatgaacc ttgtctacta aaaatacaaa 750  
 aaattagcca ggcacagtgg tgtgcactgg tagtccaggt tactcgaggag 800  
 gctgaggcag gaaaatcgct tgaaccocagg aggcgggacgt tgcggtgagc 850  
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 tcacaca 907

<210> 399  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

<400> 399  
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 1 5 10 15  
 Trp Ser Leu Leu Ala Glu Arg Val Ser Trp Val Arg Asp Ala Glu  
 20 25 30  
 Asp Ala His Arg Leu Gln Pro Phe Val Thr Glu Arg Thr Leu Gly  
 35 40 45  
 Lys Val Gln Arg Trp Ser Gly Val His Thr Gln Thr Gly Gly Arg  
 50 55 60  
 Ala Gly Gly Gly Gln Phe Cys Cys Ala Trp Leu Asp Ser Lys Arg  
 65 70 75  
 Val Leu Ala Ser Pro Gly Trp Gly Ala Ala Asn Ser Ile Lys Asn  
 80 85 90  
 Gln Arg Val Trp Ala Pro Ala Thr Glu Ser Ser Ala Gln Leu Leu  
 95 100 105  
 Cys Cys Trp Pro Val Gly Val Ala Arg Gly Gly Ala Leu Cys Gln  
 110 115 120

<210> 400  
 <211> 893  
 <212> DNA  
 <213> Homo sapiens

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 aggagctgac cctgctcttc catgggaacc tgcagctggg ccaggccctc 150  
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 cctgggtctc tatggccgca caatagaact cctggggcag gaggtcagcc 250  
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tagaagtcca gctgaggagc gcctggctgg gcctgccta cggagaattt 450  
 gaggtctttaa aggtctcacgc tgacaagcag agccacatcc tatgggcctt 500  
 cacaggccac gtgcagcggc agaggcggga gatggtggca cagcagcatc 550  
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 gccaggggcg cgggccccac ttctgagcac agagcagaga cagacgcagg 750  
 cggggacaaa ggcagaggat gttagcccat tggggagggg tggagggaag 800  
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<210> 401

<211> 198

<212> PRT

<213> Homo sapiens

<400> 401

Met	Pro	Val	Pro	Ala	Leu	Cys	Leu	Leu	Trp	Ala	Leu	Ala	Met	Val
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Thr	Arg	Pro	Ala	Ser	Ala	Ala	Pro	Met	Gly	Gly	Pro	Glu	Leu	Ala
				20					25				30	
Gln	His	Glu	Glu	Leu	Thr	Leu	Leu	Phe	His	Gly	Thr	Leu	Gln	Leu
				35					40				45	
Gly	Gln	Ala	Leu	Asn	Gly	Val	Tyr	Arg	Thr	Thr	Glu	Gly	Arg	Leu
				50					55				60	
Thr	Lys	Ala	Arg	Asn	Ser	Leu	Gly	Leu	Tyr	Gly	Arg	Thr	Ile	Glu
				65					70				75	
Leu	Leu	Gly	Gln	Glu	Val	Ser	Arg	Gly	Arg	Asp	Ala	Ala	Gln	Glu
				80					85				90	
Leu	Arg	Ala	Ser	Leu	Leu	Glu	Thr	Gln	Met	Glu	Glu	Asp	Ile	Leu
				95					100				105	
Gln	Leu	Gln	Ala	Glu	Ala	Thr	Ala	Glu	Val	Leu	Gly	Glu	Val	Ala
				110					115				120	
Gln	Ala	Gln	Lys	Val	Leu	Arg	Asp	Ser	Val	Gln	Arg	Leu	Glu	Val
				125					130				135	
Gln	Leu	Arg	Ser	Ala	Trp	Leu	Gly	Pro	Ala	Tyr	Arg	Glu	Phe	Glu
				140					145				150	
Val	Leu	Lys	Ala	His	Ala	Asp	Lys	Gln	Ser	His	Ile	Leu	Trp	Ala
				155					160				165	
Leu	Thr	Gly	His	Val	Gln	Arg	Gln	Arg	Arg	Glu	Met	Val	Ala	Gln
				170					175				180	
Gln	His	Arg	Leu	Arg	Gln	Ile	Gln	Glu	Arg	Leu	His	Thr	Ala	Ala

## Leu Pro Ala

&lt;210&gt; 402

&lt;211&gt; 1915

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 402

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 aaggatggag atctgaagac tcaaatgtaa aagctctgga cagaagtcaa 200  
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cactttgcaa actttaacta cacatgcttg gaattaagtt ttagctgttt 1850  
tcattgtcga ataataaagc ctgaattctg atcaataaaa aaaaaaaaaa 1900  
aaaaaaaaa aaaaa 1915

<210> 403  
<211> 206  
<212> PRT  
<213> Homo sapiens

<400> 403  
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Val Ile Cys Ile Leu Val Ile Thr Leu Leu Leu Asp Gln Thr Thr  
20 25 30  
Ser His Thr Ser Arg Leu Lys Ala Arg Lys His Ser Lys Arg Arg  
35 40 45  
Val Arg Asp Lys Asp Gly Asp Leu Lys Thr Gln Ile Glu Lys Leu  
50 55 60  
Trp Thr Glu Val Asn Ala Leu Lys Glu Ile Gln Ala Leu Gln Thr  
65 70 75  
Val Cys Leu Arg Gly Thr Lys Val His Lys Lys Cys Tyr Leu Ala  
80 85 90  
Ser Glu Gly Leu Lys His Phe His Glu Ala Asn Glu Asp Cys Ile  
95 100 105  
Ser Lys Gly Gly Ile Leu Val Ile Pro Arg Asn Ser Asp Glu Ile  
110 115 120  
Asn Ala Leu Gln Asp Tyr Gly Lys Arg Ser Leu Pro Gly Val Asn  
125 130 135  
Asp Phe Trp Leu Gly Ile Asn Asp Met Val Thr Glu Gly Lys Phe  
140 145 150  
Val Asp Val Asn Gly Ile Ala Ile Ser Phe Leu Asn Trp Asp Arg

	155		160		165
Ala	Gln	Pro	Asn	Gly	Gly
	170	Lys	Arg	Glu	Asn
		Cys	Val	Leu	Phe
					180
Gln	Ser	Ala	Gln	Gly	Lys
	185	Trp	Ser	Asp	Glu
					190
Lys	Arg	Tyr	Ile	Cys	Glu
	200	Phe	Thr	Ile	Pro
					Lys
					205

<210> 404  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 404  
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<210> 405  
 <211> 23  
 <212> DNA  
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<220>  
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<400> 405  
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<210> 406  
 <211> 46  
 <212> DNA  
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<220>  
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<400> 406  
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<210> 407  
 <211> 570  
 <212> DNA  
 <213> Homo sapiens

<400> 407  
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ggccctgaag gccctgctgg gggccctgac agtgtttggc tgagccgaga 400  
 ctggagcatc tacacctgag gacaagacgc tgcccacccg cgagggtga 450  
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<210> 408  
 <211> 104  
 <212> PRT  
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 20 25 30  
 Gln Pro Val Ala Ala Leu Glu Ser Ala Ala Glu Ala Gly Ala Gly  
 35 40 45  
 Thr Leu Ala Asn Pro Leu Gly Thr Leu Asn Pro Leu Lys Leu Leu  
 50 55 60  
 Leu Ser Ser Leu Gly Ile Pro Val Asn His Leu Ile Glu Gly Ser  
 65 70 75  
 Gln Lys Cys Val Ala Glu Leu Gly Pro Gln Ala Val Gly Ala Val  
 80 85 90  
 Lys Ala Leu Lys Ala Leu Leu Gly Ala Leu Thr Val Phe Gly  
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<210> 409  
 <211> 2089  
 <212> DNA  
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<400> 409  
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 aactgcctca ccaaggaaat gccaccatgc tgggtgtcct catggagaaa 1000  
 atgggtgacc acctcgccct tgaagactac ctgaccacag acttgggtga 1050  
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 aagtgtatga aaggggcaact gaggcagtgg caggaaatct gtcagaaatt 1300  
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 ggagaattca catcctgggt gggacagagc aggacgatgc aagattccat 1900  
 cccactactc agaatggcat gctgcttaag acttttagat tgtttatttc 1950  
 tggaattttt catttaatgt ttttgacca tggttgacca tggtaactg 2000  
 agactgcaga aagcaaaacc atggataagg gaggactact acaaaagcat 2050  
 taaattgata catatttttt aaaaaaaaaa aaaaaaaaaa 2089

<210> 410  
 <211> 444  
 <212> PRT  
 <213> Homo sapiens

<400> 410

Met	Lys	Val	Val	Pro	Ser	Leu	Leu	Leu	Ser	Val	Leu	Leu	Ala	Gln	1	5	10	15
Val	Trp	Leu	Val	Pro	Gly	Leu	Ala	Pro	Ser	Pro	Gln	Ser	Pro	Glu	20	25	30	
Thr	Pro	Ala	Pro	Gln	Asn	Gln	Thr	Ser	Arg	Val	Val	Gln	Ala	Pro	35	40	45	
Arg	Glu	Glu	Glu	Glu	Asp	Glu	Gln	Glu	Ala	Ser	Glu	Glu	Lys	Ala	50	55	60	
Gly	Glu	Glu	Glu	Lys	Ala	Trp	Leu	Met	Ala	Ser	Arg	Gln	Gln	Leu	65	70	75	
Ala	Lys	Glu	Thr	Ser	Asn	Phe	Gly	Phe	Ser	Leu	Leu	Arg	Lys	Ile	80	85	90	
Ser	Met	Arg	His	Asp	Gly	Asn	Met	Val	Phe	Ser	Pro	Phe	Gly	Met	95	100	105	
Ser	Leu	Ala	Met	Thr	Gly	Leu	Met	Leu	Gly	Ala	Thr	Gly	Pro	Thr	110	115	120	
Glu	Thr	Gln	Ile	Lys	Arg	Gly	Leu	His	Leu	Gln	Ala	Leu	Lys	Pro	125	130	135	
Thr	Lys	Pro	Gly	Leu	Leu	Pro	Ser	Leu	Phe	Lys	Gly	Leu	Arg	Glu	140	145	150	
Thr	Leu	Ser	Arg	Asn	Leu	Glu	Leu	Gly	Leu	Ser	Gln	Gly	Ser	Phe	155	160	165	
Ala	Phe	Ile	His	Lys	Asp	Phe	Asp	Val	Lys	Glu	Thr	Phe	Phe	Asn	170	175	180	
Leu	Ser	Lys	Arg	Tyr	Phe	Asp	Thr	Glu	Cys	Val	Pro	Met	Asn	Phe	185	190	195	
Arg	Asn	Ala	Ser	Gln	Ala	Lys	Arg	Leu	Met	Asn	His	Tyr	Ile	Asn	200	205	210	
Lys	Glu	Thr	Arg	Gly	Lys	Ile	Pro	Lys	Leu	Phe	Asp	Glu	Ile	Asn	215	220	225	
Pro	Glu	Thr	Lys	Leu	Ile	Leu	Val	Asp	Tyr	Ile	Leu	Phe	Lys	Gly	230	235	240	
Lys	Trp	Leu	Thr	Pro	Phe	Asp	Pro	Val	Phe	Thr	Glu	Val	Asp	Thr	245	250	255	
Phe	His	Leu	Asp	Lys	Tyr	Lys	Thr	Ile	Lys	Val	Pro	Met	Met	Tyr	260	265	270	
Gly	Ala	Gly	Lys	Phe	Ala	Ser	Thr	Phe	Asp	Lys	Asn	Phe	Arg	Cys	275	280	285	

His Val Leu Lys Leu Pro Tyr Gln Gly Asn Ala Thr Met Leu Val  
 290 295 300  
 Val Leu Met Glu Lys Met Gly Asp His Leu Ala Leu Glu Asp Tyr  
 305 310 315  
 Leu Thr Thr Asp Leu Val Glu Thr Trp Leu Arg Asn Met Lys Thr  
 320 325 330  
 Arg Asn Met Glu Val Phe Phe Pro Lys Phe Lys Leu Asp Gln Lys  
 335 340 345  
 Tyr Glu Met His Glu Leu Leu Arg Gln Met Gly Ile Arg Arg Ile  
 350 355 360  
 Phe Ser Pro Phe Ala Asp Leu Ser Glu Leu Ser Ala Thr Gly Arg  
 365 370 375  
 Asn Leu Gln Val Ser Arg Val Leu Arg Arg Thr Val Ile Glu Val  
 380 385 390  
 Asp Glu Arg Gly Thr Glu Ala Val Ala Gly Ile Leu Ser Glu Ile  
 395 400 405  
 Thr Ala Tyr Ser Met Pro Pro Val Ile Lys Val Asp Arg Pro Phe  
 410 415 420  
 His Phe Met Ile Tyr Glu Glu Thr Ser Gly Met Leu Leu Phe Leu  
 425 430 435  
 Gly Arg Val Val Asn Pro Thr Leu Leu  
 440

<210> 411  
 <211> 636  
 <212> DNA  
 <213> Homo sapiens

<400> 411  
 ctgggcatcag ccactgcagc tccctgagca ctctctacag agacgcggac 50  
 cccagacatg aggaggctcc tccctggtcac cagcctggtg gttgtgctgc 100  
 tgtggggaggc aggtgcagtc ccagcaccca aggtccctat caagatgcaa 150  
 gtcaaacact ggccctcaga gcaggaccca gagaaggcct ggggcgcccc 200  
 tgtggtggag cctccggaga aggaagacca gctggtggtg ctgttccctg 250  
 tccagaagcc gaaactcttg accaccgagg agaagccaag aggtcagggc 300  
 aggggccccc tccttccagg caccaaggcc tggatggaga ccgaggacac 350  
 cctggggcgt gtcctgagtc ccgagccga ccatgacagc ctgtaccacc 400  
 ctccgcctga ggaggaccag ggcgaggaga ggccccggtt gtgggtgatg 450  
 ccaaatacacc aggtgctcct gggaacggag gaagaccaag accacatcta 500  
 ccacccccag tagggctcca ggggccatca ctgccccgc cctgtcccaa 550  
 ggccccaggct gttgggactg ggaccctccc taccctgccc cagctagaca 600



aataaacccc agcaggcaaa aaaaaaaaaa aaaaaa 636

<210> 412

<211> 151

<212> PRT

<213> Homo sapiens

<400> 412

Met	Arg	Arg	Leu	Leu	Val	Thr	Ser	Leu	Val	Val	Val	Leu	Leu
1			5					10				15	
Trp	Glu	Ala	Gly	Ala	Val	Pro	Ala	Pro	Lys	Val	Pro	Ile	Lys
			20					25				30	Met
Gln	Val	Lys	His	Trp	Pro	Ser	Glu	Gln	Asp	Pro	Glu	Lys	Ala
			35					40				45	Trp
Gly	Ala	Arg	Val	Val	Glu	Pro	Pro	Glu	Lys	Asp	Asp	Gln	Leu
			50					55				60	Val
Val	Leu	Phe	Pro	Val	Gln	Lys	Pro	Lys	Leu	Leu	Thr	Thr	Glu
			65					70				75	Glu
Lys	Pro	Arg	Gly	Gln	Gly	Arg	Gly	Pro	Ile	Leu	Pro	Gly	Thr
			80					85				90	Lys
Ala	Trp	Met	Glu	Thr	Glu	Asp	Thr	Leu	Gly	Arg	Val	Leu	Ser
			95					100				105	Pro
Glu	Pro	Asp	His	Asp	Ser	Leu	Tyr	His	Pro	Pro	Pro	Glu	Glu
			110					115				120	Asp
Gln	Gly	Glu	Glu	Arg	Pro	Arg	Leu	Trp	Val	Met	Pro	Asn	His
			125					130				135	Gln
Val	Leu	Leu	Gly	Pro	Glu	Glu	Asp	Gln	Asp	His	Ile	Tyr	His
			140					145				150	Pro
Gln													

<210> 413

<211> 1176

<212> DNA

<213> Homo sapiens

<400> 413

agaaagctgc actctgttga gctccagggc gcagtgaggagg gagggagtga 50  
aggagctctc tgtacccaag gaaagtgcag ctgagactca gacaagatta 100  
caatgaacca actcagcttc ctgctgtttc tcatagcgac caccagagga 150  
tggagtacag atgaggctaa tacttacttc aaggaatgga cctgttcttc 200  
gtctccatct ctgccagaa gctgcaagga aatcaaagac gaatgtccta 250  
gtgcatttga tggcctgtat tttctcogca ctgagaatgg tggtatctac 300  
cagaccttct gtgacatgac ctctgggggt ggcggctgga ccctggtggc 350  
cagcgtgcat gagaatgaca tgcgtgggaa gtgcacgggt ggcgatcgct 400

ggtccagtcg gcagggcagc aaagcagact acccagaggg ggacggcaac 450  
 tggggccaaact acaacacctt tggatctgca gaggcggcca cgagcgatga 500  
 ctacaagaac cctggctact acgacatcca ggccaaggac ctgggcatct 550  
 ggacgctgcc caataagtcc cccatgcagc actggagaaa cagctccctg 600  
 ctgagggtacc gcacggacac tggcttctcc cagacactgg gacataatct 650  
 gtttggtatc taccagaaat atccagtga atatggagaa ggaaagtgtt 700  
 ggactgacaa cggcccgggtg atccctgtgg tctatgattt tggcgacgcc 750  
 cagaaaacag catcttatta ctcacctat ggccagcggg aattcaactgc 800  
 gggatttgtt cagttcaggg tatttaataa cgagagagca gccaacgcct 850  
 tgtgtgctgg aatgagggtc accggatgta acactgagca tcaactgcatt 900  
 ggtggaggag gatactttcc agaggccagt ccccgagcgt gtggagattt 950  
 ttctggtttt gattggagtg gatattgaac tcatgttgtt tacagcagca 1000  
 gcgtgagat aactgaggca gctgtgcttc tattctatcg ttgagagttt 1050  
 tgtggggagg aaccagacc tctctccca accatgagat cccaaggatg 1100  
 gagaacaact taccagtag ctagaatgtt aatggcagaa gagaaaacaa 1150  
 taaatcatat tgactcaaga aaaaaa 1176

<210> 414

<211> 313

<212> PRT

<213> Homo sapiens

<400> 414

Met	Asn	Gln	Leu	Ser	5	Phe	Leu	Leu	Phe	Leu	10	Ile	Ala	Thr	Thr	Arg	15
Gly	Trp	Ser	Thr	Asp	20	Glu	Ala	Asn	Thr	Tyr	25	Phe	Lys	Glu	Trp	Thr	30
Cys	Ser	Ser	Ser	Pro	35	Ser	Leu	Pro	Arg	Ser	40	Cys	Lys	Glu	Ile	Lys	45
Asp	Glu	Cys	Pro	Ser	50	Ala	Phe	Asp	Gly	Leu	55	Tyr	Phe	Leu	Arg	Thr	60
Glu	Asn	Gly	Val	Ile	65	Tyr	Gln	Thr	Phe	Cys	70	Asp	Met	Thr	Ser	Gly	75
Gly	Gly	Gly	Trp	Thr	80	Leu	Val	Ala	Ser	Val	85	His	Glu	Asn	Asp	Met	90
Arg	Gly	Lys	Cys	Thr	95	Val	Gly	Asp	Arg	Trp	100	Ser	Ser	Gln	Gln	Gly	105
Ser	Lys	Ala	Asp	Tyr	110	Pro	Glu	Gly	Asp	Gly	115	Asn	Trp	Ala	Asn	Tyr	120
Asn	Thr	Phe	Gly	Ser		Ala	Glu	Ala	Ala	Thr		Ser	Asp	Asp	Tyr	Lys	

	125		130		135
Asn Pro Gly Tyr	Tyr Asp Ile Gln Ala	Lys Asp Leu Gly Ile	Trp		
	140		145		150
His Val Pro Asn	Lys Ser Pro Met Gln	His Trp Arg Asn Ser	Ser		
	155		160		165
Leu Leu Arg Tyr	Arg Thr Asp Thr Gly	Phe Leu Gln Thr Leu	Gly		
	170		175		180
His Asn Leu Phe	Gly Ile Tyr Gln Lys	Tyr Pro Val Lys Tyr	Gly		
	185		190		195
Glu Gly Lys Cys	Trp Thr Asp Asn Gly	Pro Val Ile Pro Val	Val		
	200		205		210
Tyr Asp Phe Gly	Asp Ala Gln Lys Thr	Ala Ser Tyr Tyr Ser	Pro		
	215		220		225
Tyr Gly Gln Arg	Glu Phe Thr Ala Gly	Phe Val Gln Phe Arg	Val		
	230		235		240
Phe Asn Asn Glu	Arg Ala Ala Asn Ala	Leu Cys Ala Gly Met	Arg		
	245		250		255
Val Thr Gly Cys	Asn Thr Glu His His	Cys Ile Gly Gly Gly	Gly		
	260		265		270
Tyr Phe Pro Glu	Ala Ser Pro Gln Gln	Cys Gly Asp Phe Ser	Gly		
	275		280		285
Phe Asp Trp Ser	Gly Tyr Gly Thr His	Val Gly Tyr Ser Ser	Ser		
	290		295		300
Arg Glu Ile Thr	Glu Ala Ala Val Leu	Leu Phe Tyr Arg			
	305		310		

<210> 415

<211> 1281

<212> DNA

<213> Homo sapiens

<400> 415

gcggagccgg cgccggctgc gcagaggagc cgctctcgcc gccgccacct 50  
 cggctgggag cccacgaggc tgcgcgatcc tgccctcgga acaatgggac 100  
 tcggcgcgcg aggtgcttgg gccgcgctgc tcttggggac gctgcagggtg 150  
 cttagcgctgc tgggggcccgc ccatgaaagc gcagccatgg cggcatctgc 200  
 aaacatagag aattctgggc ttccacacaa ctccagtgcct aactcaacag 250  
 agactctcca acatgtgcct tctgaccata caaatgaaac ttccaacagt 300  
 actgtgaaac caccaacttc agttgcctca gactccagta atacaacggt 350  
 caccaccatg aaacctacag cggcatctaa tacaacaaca ccagggatgg 400  
 ttctacaaca tatgacttct accaccttaa agtctacacc caaaacaaca 450  
 agtggtttcac agaacacatc tcagatatca acatccacaa tgaccgtaac 500

ccacaatagt tcagtgacat ctgctgcttc atcagtaaca atcacaacaa 550  
 ctatgcattc tgaagcaaaag aaaggatcaa aatttgatag tgggagcttt 600  
 gttggtggta ttgtattaac gctgggagtt ttatctattc ttacattgg 650  
 atgcaaaatg tattactcaa gaagaggcat tcggtatcga accatagatg 700  
 aacatgatgc catcatttaa ggaaatccat ggaccaagga tggataacag 750  
 attgatgctg cccatcaat taattttggt ttattaatag tttaaaca 800  
 tattctcttt ttgaaaatag tataaacagg ccatgcatat aatgtacagt 850  
 gtattacgta aatatgtaaa gattcttcaa ggtaacaagg gtttgggttt 900  
 tgaaataaac atctggatct tatagaccgt tcatacaatg gttttagcaa 950  
 gttcatagta agacaaacaa gtcctatctt tttttttgg ctgggggtgg 1000  
 ggcattggtc acatatgacc agtaattgaa agacgtcatc actgaaagac 1050  
 agaatgccat ctgggcatac aaataagaag ttgtcacag cactcaggat 1100  
 tttgggtatc tttttagct cacataaaga acttcagtgc ttttcagagc 1150  
 tggatatatc ttaattacta atgccacaca gaaattatac aatcaaaacta 1200  
 gatctgaagc ataatttaag aaaaacatca acattttttg tgcctttaac 1250  
 tgtagtagtt ggtctagaaa caaaatactc c 1281

<210> 416

<211> 208

<212> PRT

<213> Homo sapiens

<400> 416

Met Gly Leu Gly Ala Arg Gly Ala Trp Ala Ala Leu Leu Leu Gly	1	5	10	15
Thr Leu Gln Val Leu Ala Leu Leu Gly Ala Ala His Glu Ser Ala	20	25	30	
Ala Met Ala Ala Ser Ala Asn Ile Glu Asn Ser Gly Leu Pro His	35	40	45	
Asn Ser Ser Ala Asn Ser Thr Glu Thr Leu Gln His Val Pro Ser	50	55	60	
Asp His Thr Asn Glu Thr Ser Asn Ser Thr Val Lys Pro Pro Thr	65	70	75	
Ser Val Ala Ser Asp Ser Ser Asn Thr Thr Val Thr Thr Met Lys	80	85	90	
Pro Thr Ala Ala Ser Asn Thr Thr Thr Pro Gly Met Val Ser Thr	95	100	105	
Asn Met Thr Ser Thr Thr Leu Lys Ser Thr Pro Lys Thr Thr Ser	110	115	120	
Val Ser Gln Asn Thr Ser Gln Ile Ser Thr Ser Thr Met Thr Val				

125	130	135
Thr His Asn Ser Ser Val Thr Ser Ala	Ala Ser Ser Val Thr Ile	
140	145	150
Thr Thr Thr Met His Ser Glu Ala Lys	Lys Gly Ser Lys Phe Asp	
155	160	165
Thr Gly Ser Phe Val Gly Gly Ile Val	Leu Thr Leu Gly Val Leu	
170	175	180
Ser Ile Leu Tyr Ile Gly Cys Lys Met	Tyr Tyr Ser Arg Arg Gly	
185	190	195
Ile Arg Tyr Arg Thr Ile Asp Glu His	Asp Ala Ile Ile	
200	205	

<210> 417  
 <211> 1728  
 <212> DNA  
 <213> Homo sapiens

<400> 417  
 cagccgggtc ccaagcctgt gcctgagcct gagcctgagc ctgagcccca 50  
 gccgggagcc ggtcgcgggg gctccgggct gtgggaccgc tgggccccca 100  
 gcgatggcga ccctgtgggg aggccttctt cgcttggtct ccttgctcag 150  
 cctgtcgtgc ctggcgcttt ccgtgctgct gctggcgagc ctgtcagacg 200  
 ccgccaagaa ttctgaggat gtcagatgta aatgtatctg cctccctat 250  
 aaagaaaatt ctgggcataa ttataataag aacatatctc agaaagattg 300  
 tgattgcctt catgttggtg agcccatgcc tgtgcggggg cctgatgtag 350  
 aagcatactg tctacgctgt gaatgcaaat atgaagaaag aagctctgtc 400  
 acaatcaagg ttaccattat aatttatctc tccattttgg gccttctact 450  
 tctgtacatg gtatatctta ctctggttga gcccatactg aagaggcgcc 500  
 tctttggaca tgcacagttg atacagagtg atgatgat atggggatcac 550  
 cagccttttg caaatgcaca cgaatgtgcta gcccgctccc gcagtcgagc 600  
 caacgtgctg aacaaggtag aatatgcaca gcagcgctgg aagcttcaag 650  
 tccaagagca gcaaaagtct gtctttgacc ggcattgtgt cctcagctaa 700  
 ttgggaattg aattcaagg gactagaaag aaacaggcag acaactggaa 750  
 agaactgact gggttttgct gggtttcatt ttaataacct gttgatttca 800  
 ccaactgttg ctggaagatt caaaactgga agcaaaaaact tgcttgattt 850  
 ttttttcttg ttaacgtaat aatagagaca tttttaaaag cacacagctc 900  
 aaagtcagcc aataagtctt ttctatttg tgacttttac taataaaaat 950  
 aaatctgcct gtaaattatc ttgaagtcct ttacctgaa caagcactct 1000

ctttttcacc acatagtttt aacttgactt tcaagataat tttcagggtt 1050  
 ttgttggttg ttgttttttg tttgtttggt ttgggtgggag agggggaggga 1100  
 tgcctgggaa gtggttaaca actttttttca agtcacttta ctaaacaac 1150  
 ttttgtaaat agaccttacc ttctattttc gagtttcatt tatattttgc 1200  
 agtgtagcca gctcatcaa agagctgact tactcatttg acttttgcac 1250  
 tgaactgtatt atctgggtat ctgctgtgtc tgcacttcat ggtaaacggg 1300  
 atctaaaatg cctgggtggct tttcacaaaa agcagatttt cttcatgtac 1350  
 tgtgatgtct gatgcaatgc atcctagaac aaactggcca tttgctagtt 1400  
 tactctaaag actaaacata gtcttggtgt gtgtgggtctt actcatcttc 1450  
 tagtaccttt aagacaaaat cctaaggact tggacacttg caataaagaa 1500  
 attttatttt aaaccaagc ctccctggat tgataatata tacacatttg 1550  
 tcagcatttc cggctgtggt gagaggcagc tgtttgagct ccaatatgtg 1600  
 cagctttgaa ctagggtctgg ggttggtgggt gcctcttctg aaaggtctaa 1650  
 ccattattgg ataactggct tttttcttcc tatgtctctt ttggaatgta 1700  
 acaataaaaa taatttttga aacatcaa 1728

<210> 418

<211> 198

<212> PRT

<213> Homo sapiens

<400> 418

Met	Ala	Thr	Leu	Trp	Gly	Gly	Leu	Leu	Arg	Leu	Gly	Ser	Leu	Leu
1				5					10					15
Ser	Leu	Ser	Cys	Leu	Ala	Leu	Ser	Val	Leu	Leu	Leu	Ala	Gln	Leu
				20					25					30
Ser	Asp	Ala	Ala	Lys	Asn	Phe	Glu	Asp	Val	Arg	Cys	Lys	Cys	Ile
				35					40					45
Cys	Pro	Pro	Tyr	Lys	Glu	Asn	Ser	Gly	His	Ile	Tyr	Asn	Lys	Asn
				50					55					60
Ile	Ser	Gln	Lys	Asp	Cys	Asp	Cys	Leu	His	Val	Val	Glu	Pro	Met
				65					70					75
Pro	Val	Arg	Gly	Pro	Asp	Val	Glu	Ala	Tyr	Cys	Leu	Arg	Cys	Glu
				80					85					90
Cys	Lys	Tyr	Glu	Glu	Arg	Ser	Ser	Val	Thr	Ile	Lys	Val	Thr	Ile
				95					100					105
Ile	Ile	Tyr	Leu	Ser	Ile	Leu	Gly	Leu	Leu	Leu	Tyr	Met	Val	
				110					115				120	
Tyr	Leu	Thr	Leu	Val	Glu	Pro	Ile	Leu	Lys	Arg	Arg	Leu	Phe	Gly
				125					130					135

His Ala Gln Leu Ile Gln Ser Asp Asp Asp Ile Gly Asp His Gln  
 140 145 150  
 Pro Phe Ala Asn Ala His Asp Val Leu Ala Arg Ser Arg Ser Arg  
 155 160 165  
 Ala Asn Val Leu Asn Lys Val Glu Tyr Ala Gln Gln Arg Trp Lys  
 170 175 180  
 Leu Gln Val Gln Glu Gln Arg Lys Ser Val Phe Asp Arg His Val  
 185 190 195  
 Val Leu Ser

<210> 419  
 <211> 681  
 <212> DNA  
 <213> Homo sapiens

<400> 419  
 gcacctgcca ccacctgag cagtcatggc gtactccaca gtgcagagag 50  
 tcgctctggc ttctgggctt gtccctggctc tgcctgtgct gctgcccaag 100  
 gccttctctgt cccgcgggaa gcgcgaggag ccgcccgca cacctgaagg 150  
 aaaattgggc cgatttcac ctatgatgca tcatccacag gcacctcag 200  
 atggccagac tcctggggct cgtttccaga ggtctcacct tgccgaggca 250  
 ttgcaaaagg ccaaaggatc aggtggagggt gctggaggag gaggtagtgg 300  
 aagagggtctg atggggcaga ttattccaat ctacggtttt gggatttttt 350  
 tatatatact gtacattcta tttaaggtaa gtagaatcat cctaatacata 400  
 ttacatcaat gaaaatctaa tatggcgata aaaatcattg tctacattaa 450  
 aacttcctat agttcataaa attatttcaa atccatcatc tctttaaatc 500  
 ctgcctcttc ttcagtaggt acttaggata gccattatct cagtttcaca 550  
 taagaatggt tactcaatgt ttaagtgttt tgcccaaaaa ttcacaacta 600  
 acaaggcaga actaggactt gaacatggat cttttgggtc ttaatcoagt 650  
 gagtgtatata attcaatgca ctcccctgcc a 681

<210> 420  
 <211> 128  
 <212> PRT  
 <213> Homo sapiens

<400> 420  
 Met Ala Tyr Ser Thr Val Gln Arg Val Ala Leu Ala Ser Gly Leu  
 1 5 10 15  
 Val Leu Ala Leu Ser Leu Leu Leu Pro Lys Ala Phe Leu Ser Arg  
 20 25 30  
 Gly Lys Arg Gln Glu Pro Pro Pro Thr Pro Glu Gly Lys Leu Gly  
 35 40 45

Arg	Phe	Pro	Pro	Met	Met	His	His	His	Gln	Ala	Pro	Ser	Asp	Gly
				50					55					60
Gln	Thr	Pro	Gly	Ala	Arg	Phe	Gln	Arg	Ser	His	Leu	Ala	Glu	Ala
				65					70					75
Phe	Ala	Lys	Ala	Lys	Gly	Ser	Gly	Gly	Gly	Ala	Gly	Gly	Gly	Gly
				80					85					90
Ser	Gly	Arg	Gly	Leu	Met	Gly	Gln	Ile	Ile	Pro	Ile	Tyr	Gly	Phe
				95					100					105
Gly	Ile	Phe	Leu	Tyr	Ile	Leu	Tyr	Ile	Leu	Phe	Lys	Val	Ser	Arg
				110					115					120
Ile	Ile	Leu	Ile	Ile	Leu	His	Gln							
				125										

<210> 421  
 <211> 1630  
 <212> DNA  
 <213> Homo sapiens

<400> 421  
 cggtctcgagt gcagctgtgg ggagatttca gtgcattgcc tccccgggt 50  
 gctcttcato ttgatttga aagttgagag cagcatgttt tgccactga 100  
 aactcatcct gctgccagt ttactggatt attccttggg cctgaatgac 150  
 ttgaatgttt ccccgctga gctaacagtc catgtgggtg attcagctct 200  
 gatgggatgt gttttccaga gcacagaaga caaatgtata ttcaagatag 250  
 actggactct gtcaccagga gagcacgcca aggacgaata tgtgtatata 300  
 tattactcca atctcagtg gcctattggg cgcttccaga accgcgtaca 350  
 cttagtgggg gacatcttat gcaatgatgg ctctctcctg ctccaagatg 400  
 tgcaagaggg tgaccagggg acctatatct gtgaaatccg cctcaaaggg 450  
 gagagccagg tgttcaagaa ggcggtggta ctgcatgtgc ttccagagga 500  
 gcccaaagag ctcatgggtc atgtgggtgg attgattcag atgggatgtg 550  
 ttttccagag cacagaagtg aaacacgtga ccaaggtaga atggatattt 600  
 tcaggacggc gcgcaaagga ggagattgta ttctgttact accacaaact 650  
 caggatgtct gtggagtact ccagagctg gggccacttc cagaatcgtg 700  
 tgaacctggt gggggacatt ttccgcaatg acggttccat catgcttcaa 750  
 ggagtgaggg agtcagatgg aggaaactac acctgcagta tccacctagg 800  
 gaacctggtg ttcaagaaaa ccattgtgct gcatgtcagc cgggaagagc 850  
 ctcgaaactt ggtgaccccg gcagccctga ggccctcgtt cttgggtggt 900  
 aatcagttgg tgatcattgt ggggaattgtc tgtgccacaa tctctgtcgt 950  
 ccctgttctg atattgatcg tgaagaagac ctgtggaaat aagagttcag 1000



tgaattctac agtcttggtg aagaacacga agaagactaa tccagagata 1050  
 aaagaaaaac cctgccattt tgaagatgt gaaggggaga aacacattta 1100  
 ctccccata attgtacggg aggtgatcga ggaagaagaa ccaagtga 1150  
 aatcagaggc cacctacatg accatgcacc cagtttgccc ttctctgagg 1200  
 tcagatcgga acaactcact tgaaaaaaag tcaggtgggg gaatgccaaa 1250  
 aacacagcaa gccttttgag aagaatggag agtccctca tctcagcagc 1300  
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 agactccgc tctccagct gtctctctgt ctctattgtt ggtcaatata 1400  
 ctgaagatgg agaatttga gcctggcaga gagactggac agctctggag 1450  
 gaacaggcct gctgagggga ggggagcatg gacttggcct ctggagtggg 1500  
 acactggccc tgggaaccag gctgagctga gtggcctcaa acccccggtt 1550  
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 Thr Val His Val Gly Asp Ser Ala Leu Met Gly Cys Val Phe Gln  
 35 40 45  
 Ser Thr Glu Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser  
 50 55 60  
 Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser  
 65 70 75  
 Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg Val His Leu  
 80 85 90  
 Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu Gln Asp  
 95 100 105  
 Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg Leu  
 110 115 120  
 Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val  
 125 130 135  
 Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu  
 140 145 150  
 Ile Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val

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Thr Lys Val Glu Trp	Ile Phe Ser Gly	Arg Arg Ala Lys Glu			
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Ile Val Phe Arg Tyr	Tyr His Lys Leu	Arg Met Ser Val Glu Tyr			
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Ser Gln Ser Trp Gly	His Phe Gln Asn	Arg Val Asn Leu Val Gly			
200		205			210
Asp Ile Phe Arg Asn	Asp Gly Ser Ile	Met Leu Gln Gly Val Arg			
215		220			225
Glu Ser Asp Gly Gly	Asn Tyr Thr Cys	Ser Ile His Leu Gly Asn			
230		235			240
Leu Val Phe Lys Lys	Thr Ile Val Leu	His Val Ser Pro Glu Gly			
245		250			255
Pro Arg Thr Leu Val	Thr Pro Ala Ala	Leu Arg Pro Leu Val Leu			
260		265			270
Gly Gly Asn Gln Leu	Val Ile Ile Val	Gly Ile Val Cys Ala Thr			
275		280			285
Ile Leu Leu Leu Pro	Val Leu Ile Leu	Ile Val Lys Lys Thr Cys			
290		295			300
Gly Asn Lys Ser Ser	Val Asn Ser Thr	Val Leu Val Lys Asn Thr			
305		310			315
Lys Lys Thr Asn Pro	Glu Ile Lys Glu	Lys Pro Cys His Phe Glu			
320		325			330
Arg Cys Glu Gly Glu	Lys His Ile Tyr	Ser Pro Ile Ile Val Arg			
335		340			345
Glu Val Ile Glu Glu	Glu Glu Pro Ser	Glu Lys Ser Glu Ala Thr			
350		355			360
Tyr Met Thr Met His	Pro Val Trp Pro	Ser Leu Arg Ser Asp Arg			
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Gln Gln Ala Phe					

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<213> Homo sapiens

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ctctgagctc agttgcagta ctcggaagc catgcaggat gaagatggat 200

acatcacctt aaatattaaa actcggaac cagctctcgt ctccgttggc 250  
 cctgcacccct cctcctggtg gcgtgtgatg gctttgatcc tgctgaccc 300  
 gtgcgtgggg atggttgctg ggctggtggc tctggggatt tggctctgca 350  
 tgcagcgcaa ttacctacaa gatgagaatg aaaatcgac aggaactctg 400  
 caacaattag caaagcgctt ctgtcaatat gtggtaaaac aatcagaact 450  
 aaagggcact tcaaaggtc ataatgcag cccctgtgac acaaactgga 500  
 gatattatgg agatagctgc tatgggttct tcaggcacaa cttaacatgg 550  
 gaagagagta agcagtactg cactgacatg aatgctactc toctgaagat 600  
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 gatggctcgg ttatctcaga aaatagtgtt gagtttttgg aagatggaaa 750  
 aggaaatgat aattgtgctt attttcataa tgggaaaaat caccctacct 800  
 tctgtgagaa caaacattat ttaattgtgt agaggaaggc tggcatgacc 850  
 aaggtggacc aactacctta atgcaaagag gtggacagga taacacagat 900  
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<211> 229

<212> PRT

<213> Homo sapiens

<400> 424

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			20					25						30

Arg	Val	Met	Ala	Leu	Ile	Leu	Leu	Ile	Leu	Cys	Val	Gly	Met	Val
			35					40						45

Val	Gly	Leu	Val	Ala	Leu	Gly	Ile	Trp	Ser	Val	Met	Gln	Arg	Asn
			50					55						60

Tyr	Leu	Gln	Asp	Glu	Asn	Glu	Asn	Arg	Thr	Gly	Thr	Leu	Gln	Gln
			65					70						75

Leu	Ala	Lys	Arg	Phe	Cys	Gln	Tyr	Val	Val	Lys	Gln	Ser	Glu	Leu
			80					85						90

Lys	Gly	Thr	Phe	Lys	Gly	His	Lys	Cys	Ser	Pro	Cys	Asp	Thr	Asn
			95					100						105

Trp	Arg	Tyr	Tyr	Gly	Asp	Ser	Cys	Tyr	Gly	Phe	Phe	Arg	His	Asn
			110					115						120

Leu	Thr	Trp	Glu	Glu	Ser	Lys	Gln	Tyr	Cys	Thr	Asp	Met	Asn	Ala
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125	130	135
Thr Leu Leu Lys Ile Asp Asn Arg Asn	Ile Val Glu Tyr Ile Lys	
140	145	150
Ala Arg Thr His Leu Ile Arg Trp Val	Gly Leu Ser Arg Gln Lys	
155	160	165
Ser Asn Glu Val Trp Lys Trp Glu Asp	Gly Ser Val Ile Ser Glu	
170	175	180
Asn Met Phe Glu Phe Leu Glu Asp Gly	Lys Gly Asn Met Asn Cys	
185	190	195
Ala Tyr Phe His Asn Gly Lys Met His	Pro Thr Phe Cys Glu Asn	
200	205	210
Lys His Tyr Leu Met Cys Glu Arg Lys	Ala Gly Met Thr Lys Val	
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Asp Gln Leu Pro		

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<210> 427  
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gagcccccto ctttctgaa gcccgagtgc ggagaagccc gggcaaacgc 200  
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gaggagaagg aggaggagcg gaaccagag aggggcagca aaagaagcgg 300  
tggtgtgtgg cgtcgtggcc atggcggcgg ctatcgccag ctgcctcctc 350  
cgtcagaaga ggcaagcccg cgagcgcgag aaatccaacg cctgcaagtg 400  
tgtcagcagc ccagcaaaag gcaagaccag ctgcgacaaa aacaagttaa 450  
atgtcttttc ccgggtcaaa ctcttcggct ccaagaagag gcgcagaaga 500  
agaccagagc ctcagcttaa gggatatagt accaagctat acagccgaca 550  
aggctaccac ttgcagctgc aggcggatgg aaccattgat ggcaccaaag 600  
atgaggacag cacttacact ctgtttaacc tcatccctgt gggctctcga 650  
gtgtgtggcta tccaaggagt tcaaaccaag ctgtacttgg caatgaacag 700  
tgagggatag ttgtacacct cggaactttt cacacctgag tgcaaatcca 750  
aagaatcagt gtttgaatat tattatgtga catattcctc aatgatatac 800  
cgtcagcagc agtcaggccg aggggtgtat ctgggtctga acaagaag 850  
agagatcatg aaaggcaacc atgtgaagaa gaacaagcct gcagctcatt 900



ttctgcctaa accactgaaa gtggccatgt acaaggagcc atcactgcac 950  
gatctcaccg agttctcccc atctggaagc gggaccccaa ccaagagcag 1000  
aagtgtctct ggctgtctga acggaggcaa atccatgagc cacaatgaat 1050  
caacgtagcc agtgagggca aaagaagggc tctgtaacag aaccttacct 1100  
ccaggtgctg ttgaattctt cttagcagtc ttcacccaaa agttcaaatt 1150  
tgtcagtgac atttaccaaa caaacaggca gagttcacta ttctatctgc 1200  
cattagacct tcttatcatc cataactaaag c 1231

<210> 495  
<211> 245  
<212> PRT  
<213> Homo Sapien

<400> 495  
Met Ala Ala Ala Ile Ala Ser Ser Leu Ile Arg Gln Lys Arg Gln  
1 5 10 15  
Ala Arg Glu Arg Glu Lys Ser Asn Ala Cys Lys Cys Val Ser Ser  
20 25 30  
Pro Ser Lys Gly Lys Thr Ser Cys Asp Lys Asn Lys Leu Asn Val  
35 40 45  
Phe Ser Arg Val Lys Leu Phe Gly Ser Lys Lys Arg Arg Arg Arg  
50 55 60  
Arg Pro Glu Pro Gln Leu Lys Gly Ile Val Thr Lys Leu Tyr Ser  
65 70 75  
Arg Gln Gly Tyr His Leu Gln Leu Gln Ala Asp Gly Thr Ile Asp  
80 85 90  
Gly Thr Lys Asp Glu Asp Ser Thr Tyr Thr Leu Phe Asn Leu Ile  
95 100 105  
Pro Val Gly Leu Arg Val Val Ala Ile Gln Gly Val Gln Thr Lys  
110 115 120  
Leu Tyr Leu Ala Met Asn Ser Glu Gly Tyr Leu Tyr Thr Ser Glu  
125 130 135  
Leu Phe Thr Pro Glu Cys Lys Phe Lys Glu Ser Val Phe Glu Asn  
140 145 150  
Tyr Tyr Val Thr Tyr Ser Ser Met Ile Tyr Arg Gln Gln Gln Ser  
155 160 165  
Gly Arg Gly Trp Tyr Leu Gly Leu Asn Lys Glu Gly Glu Ile Met  
170 175 180  
Lys Gly Asn His Val Lys Lys Asn Lys Pro Ala Ala His Phe Leu  
185 190 195  
Pro Lys Pro Leu Lys Val Ala Met Tyr Lys Glu Pro Ser Leu His  
200 205 210  
Asp Leu Thr Glu Phe Ser Arg Ser Gly Ser Gly Thr Pro Thr Lys

	215		220		225
Ser Arg Ser Val Ser Gly Val Leu Asn Gly Gly Lys Ser Met Ser					
	230		235		240
His Asn Glu Ser Thr					
	245				

<210> 496  
 <211> 1471  
 <212> DNA  
 <213> Homo Sapien

<400> 496  
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 gagccctgtc ttactgaacc tgggcaacct ggatattctg agacatatatt 150  
 tggggggatt tcagtgaaaa aagtggggga tccctccat ttagagtgtg 200  
 gcaaaggaaa aaacaccaag gttgggttcc ttccctgacat tggcagtgcc 250  
 ccagtagggg tgggatgagc gaattattccc aaagctaaag tcccacaccc 300  
 tgtagattac aagagtggat ttggcaggag tgtgcccca aatacagtgg 350  
 aaaggtgcct gaagatatatt aaaccacgtc ttggaattt agtgggtcct 400  
 ggctttggga tagtggaagt gaggacagac actggagagg agggaaagg 450  
 gacgttttca ataggaggca aaactcagg gtgggatcca ctgaggagta 500  
 cataggctgc tggatctggt ggagccagca ctgggccac ggggtgtaac 550  
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 aactgttctg ccgcaggggt ttctacctcc aggcgaatcc cgacggaagc 1000  
 atccagggca cccagagga taccagctcc ttcacccact tcaacctgat 1050  
 ccctgtgggc ctccgtgtgg tcaccatcca gagcgccaag ctgggtcact 1100  
 acatggccat gaatgctgag ggactgtctc acagtctgcc gcatttcaca 1150  
 gctgagtgtc gctttaagga gtgtgtcttt gagaattact acgtcctgta 1200  
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gacctggacaa ggagggccag gtcacgaagg gaaaccgagt taagaagacc 1300  
aaggcagctg cccactttct gcccaagctc ctggaggtgg ccatgtacca 1350  
ggagccttct ctccacagtg tccccgaggc ctccccctcc agtccccctg 1400  
ccccctgaaa tgtagtccct ggactggagg ttcctgcac tcccagtgag 1450  
ccagccacca ccacaacctg t 1471

<210> 497  
<211> 225  
<212> PRT  
<213> Homo Sapien

<400> 497  
Met Ala Ala Leu Ala Ser Ser Leu Ile Arg Gln Lys Arg Glu Val  
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Arg Glu Pro Gly Gly Ser Arg Pro Val Ser Ala Gln Arg Arg Val  
20 25 30  
Cys Pro Arg Gly Thr Lys Ser Leu Cys Gln Lys Gln Leu Leu Ile  
35 40 45  
Leu Leu Ser Lys Val Arg Leu Cys Gly Gly Arg Pro Ala Arg Pro  
50 55 60  
Asp Arg Gly Pro Glu Pro Gln Leu Lys Gly Ile Val Thr Lys Leu  
65 70 75  
Phe Cys Arg Gln Gly Phe Tyr Leu Gln Ala Asn Pro Asp Gly Ser  
80 85 90  
Ile Gln Gly Thr Pro Glu Asp Thr Ser Ser Phe Thr His Phe Asn  
95 100 105  
Leu Ile Pro Val Gly Leu Arg Val Val Thr Ile Gln Ser Ala Lys  
110 115 120  
Leu Gly His Tyr Met Ala Met Asn Ala Glu Gly Leu Leu Tyr Ser  
125 130 135  
Ser Pro His Phe Thr Ala Glu Cys Arg Phe Lys Glu Cys Val Phe  
140 145 150  
Glu Asn Tyr Tyr Val Leu Tyr Ala Ser Ala Leu Tyr Arg Gln Arg  
155 160 165  
Arg Ser Gly Arg Ala Trp Tyr Leu Gly Leu Asp Lys Glu Gly Gln  
170 175 180  
Val Met Lys Gly Asn Arg Val Lys Lys Thr Lys Ala Ala Ala His  
185 190 195  
Phe Leu Pro Lys Leu Leu Glu Val Ala Met Tyr Gln Glu Pro Ser  
200 205 210  
Leu His Ser Val Pro Glu Ala Ser Pro Ser Ser Pro Pro Ala Pro  
215 220 225

<210> 498  
<211> 744

<212> DNA  
<213> Homo Sapien

<400> 498  
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ggagcagcac tgggaccggc cgtctgccag caggaggcgg agcagcccca 100  
gcaagaaccg cgggctctgc aacggcaacc tgggtgatat ctctccaaa 150  
gtgcgcattc tcggcctcaa gaagcgagg ttgcggcgcc aagatcccca 200  
gctcaagggt atagtacca ggttatattg caggcaaggc tactacttgc 250  
aatgcacccc cgatggagct ctogattgaa ccaaggatga cagcactaat 300  
tctacattct tcaacctcat accagtggga ctacgtgttg ttgccatcca 350  
gggagtgaac acagggttgt atatatccat gaattggaga ggtacctct 400  
accatcaga actttttacc cctgaatgca agtttaaaga atctgttttt 450  
gaaaattatt atgtaatcta ctcatccatg ttgtacagac aacaggaatc 500  
tggtagagcc tggtttttgg gattaaataa ggaagggcaa gctatgaaag 550  
ggaacagagt aaagaaaacc aaaccagcag ctcattttct acccaagcca 600  
ttggaagtgt ccatgtaccg agaaccatct ttgcatgatg ttggggaaac 650  
ggtcccgag cctggggtga cgccaagtaa aagcacaagt gcgtctgcaa 700  
taatgaatgg aggcacaacca ctcaacaaga gtaagacaac atag 744

<210> 499  
<211> 247  
<212> PRT  
<213> Homo Sapien

<400> 499  
Met Ala Ala Ala Ile Ala Ser Gly Leu Ile Arg Gln Lys Arg Gln  
1 5 10 15  
Ala Arg Glu Gln His Trp Asp Arg Pro Ser Ala Ser Arg Arg Arg  
20 25 30  
Ser Ser Pro Ser Lys Asn Arg Gly Leu Cys Asn Gly Asn Leu Val  
35 40 45  
Asp Ile Phe Ser Lys Val Arg Ile Phe Gly Leu Lys Lys Arg Arg  
50 55 60  
Leu Arg Arg Gln Asp Pro Gln Leu Lys Gly Ile Val Thr Arg Leu  
65 70 75  
Tyr Cys Arg Gln Gly Tyr Tyr Leu Gln Met His Pro Asp Gly Ala  
80 85 90  
Leu Asp Gly Thr Lys Asp Asp Ser Thr Asn Ser Thr Leu Phe Asn  
95 100 105  
Leu Ile Pro Val Gly Leu Arg Val Val Ala Ile Gln Gly Val Lys  
110 115 120

Thr Gly Leu Tyr Ile Ala Met Asn Gly Glu Gly Tyr Leu Tyr Pro  
 125 130 135  
 Ser Glu Leu Phe Thr Pro Glu Cys Lys Phe Lys Glu Ser Val Phe  
 140 145 150  
 Glu Asn Tyr Tyr Val Ile Tyr Ser Ser Met Leu Tyr Arg Gln Gln  
 155 160 165  
 Glu Ser Gly Arg Ala Trp Phe Leu Gly Leu Asn Lys Glu Gly Gln  
 170 175 180  
 Ala Met Lys Gly Asn Arg Val Lys Lys Thr Lys Pro Ala Ala His  
 185 190 195  
 Phe Leu Pro Lys Pro Leu Glu Val Ala Met Tyr Arg Glu Pro Ser  
 200 205 210  
 Leu His Asp Val Gly Glu Thr Val Pro Lys Pro Gly Val Thr Pro  
 215 220 225  
 Ser Lys Ser Thr Ser Ala Ser Ala Ile Met Asn Gly Gly Lys Pro  
 230 235 240  
 Val Asn Lys Ser Lys Thr Thr  
 245

<210> 500

<211> 2906

<212> DNA

<213> Homo Sapien

<400> 500

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 tggaaccgaa cgcaatggat aaactgattg tgcaagagag aaggaagaac 150  
 gaagcttttt cttgtgagcc ctggatctta acacaaatgt gtatatgtgc 200  
 acacagggag cattcaagaa tgaataaac cagagttaga cccgcggggg 250  
 ttgtgtgtgt ctgacataaa taaataatct taaagcagct gttcccctcc 300  
 ccacccccaa aaaaaaggat gattggaat gaagaaccga ggattcacia 350  
 agaaaaaagt atgttcattt ttctctataa aggagaaagt gagccaagga 400  
 gatatttttg gaatgaaaag tttggggctt ttttagtaaa gtaaagaact 450  
 ggtgtggtgg tgttttctt tctttttgaa tttccacaa gaggagagga 500  
 aattaataat acatctgcaa agaaatttca gagaagaaaa gttgaccgcg 550  
 gcagattgag gcattgattg ggggagagaa accagcagag cacagtgtga 600  
 tttgtgccta tgttgactaa aattgacgga taattgcagt tggatttttc 650  
 ttcacaaacc tctttttttt taaattttta ttccttttgg tatcaagatc 700  
 atgcgttttc tctgttctt aaccacctgg atttccatct ggatgtgtgt 750

gtgatcagtc tgaaatacaa ctgtttgaat tccagaagga ccaacaccag 800  
 ataaattatg aatgttgaac aagatgacct tacatccaca gcagataatg 850  
 ataggctcta gggttaacag ggccctatctt gacccccctgc ttgtgggtgct 900  
 gctggctctt caactctctg tgggtggctgg tctgggtcgg gctcagacct 950  
 gcccttctgt gtgctcctgc agcaaccagt tcagcaaggt gattttgtgtt 1000  
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 agcacttgag gcacttgga atcctacagt tgagttaggaa ccatatcaga 1150  
 accattgaaa ttggggcttt caatggtctg gcgaacctca acactctgga 1200  
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 tgtctaaact gaaggagctc tggttgcgaa acaaccccat tgaaagcatc 1300  
 ccttcttatg cttttaacag aattccttct ttgcgccag tagacttagg 1350  
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 aacctcacac cgctcataaa actagatgag ctggatcttt ctgggaatca 1500  
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 gacaaccttc agtccactgt ggagatcaac ctggcacaca ataactaac 1650  
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 acaaatgtaa ctgtgcaaga tacaggcatg tacacatgta tgggtagtaa 2100  
 ttccgttggy aatactactg cttcagccac cctgaatgtt actgcagcaa 2150  
 ccactactcc tttctcttac ttttcaaccg tcacagttaga gactattgaa 2200  
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 gcacaaggtc gacagagaaa accttcacca tccagtgac tgatataaac 2350

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 ctctaaagac aatgtacaag agactcaaat ctaaaacatt tacagagtta 2750  
 caaaaaaaca acaatcaaaa aaaaagacag tttattaaaa atgacacaaa 2800  
 tgactgggct aaatctactg tttcaaaaaa gtgtctttac aaaaaacaaa 2850  
 aaaagaaaag aaattttatt attaaaaatt ctattgtgat ctaaagcaga 2900  
 caaaaa 2906

<210> 501  
 <211> 640  
 <212> PRT  
 <213> Homo Sapien

<400> 501  
 Met Leu Asn Lys Met Thr Leu His Pro Gln Gln Ile Met Ile Gly  
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 Pro Arg Phe Asn Arg Ala Leu Phe Asp Pro Leu Leu Val Val Leu  
 20 25 30  
 Leu Ala Leu Gln Leu Leu Val Val Ala Gly Leu Val Arg Ala Gln  
 35 40 45  
 Thr Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val  
 50 55 60  
 Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser  
 65 70 75  
 Thr Asn Thr Arg Leu Leu Asn Leu His Glu Asn Gln Ile Gln Ile  
 80 85 90  
 Ile Lys Val Asn Ser Phe Lys His Leu Arg His Leu Glu Ile Leu  
 95 100 105  
 Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe  
 110 115 120  
 Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg  
 125 130 135  
 Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu  
 140 145 150  
 Lys Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser  
 155 160 165

Tyr	Ala	Phe	Asn	Arg	Ile	Pro	Ser	Leu	Arg	Arg	Leu	Asp	Leu	Gly	170	175	180
Glu	Leu	Lys	Arg	Leu	Ser	Tyr	Ile	Ser	Glu	Gly	Ala	Phe	Glu	Gly	185	190	195
Leu	Ser	Asn	Leu	Arg	Tyr	Leu	Asn	Leu	Ala	Met	Cys	Asn	Leu	Arg	200	205	210
Glu	Ile	Pro	Asn	Leu	Thr	Pro	Leu	Ile	Lys	Leu	Asp	Glu	Leu	Asp	215	220	225
Leu	Ser	Gly	Asn	His	Leu	Ser	Ala	Ile	Arg	Pro	Gly	Ser	Phe	Gln	230	235	240
Gly	Leu	Met	His	Leu	Gln	Lys	Leu	Trp	Met	Ile	Gln	Ser	Gln	Ile	245	250	255
Gln	Val	Ile	Glu	Arg	Asn	Ala	Phe	Asp	Asn	Leu	Gln	Ser	Leu	Val	260	265	270
Glu	Ile	Asn	Leu	Ala	His	Asn	Asn	Leu	Thr	Leu	Leu	Pro	His	Asp	275	280	285
Leu	Phe	Thr	Pro	Leu	His	His	Leu	Glu	Arg	Ile	His	Leu	His	His	290	295	300
Asn	Pro	Trp	Asn	Cys	Asn	Cys	Asp	Ile	Leu	Trp	Leu	Ser	Trp	Trp	305	310	315
Ile	Lys	Asp	Met	Ala	Pro	Ser	Asn	Thr	Ala	Cys	Cys	Ala	Arg	Cys	320	325	330
Asn	Thr	Pro	Pro	Asn	Leu	Lys	Gly	Arg	Tyr	Ile	Gly	Glu	Leu	Asp	335	340	345
Gln	Asn	Tyr	Phe	Thr	Cys	Tyr	Ala	Pro	Val	Ile	Val	Glu	Pro	Pro	350	355	360
Ala	Asp	Leu	Asn	Val	Thr	Glu	Gly	Met	Ala	Ala	Glu	Leu	Lys	Cys	365	370	375
Arg	Ala	Ser	Thr	Ser	Leu	Thr	Ser	Val	Ser	Trp	Ile	Thr	Pro	Asn	380	385	390
Gly	Thr	Val	Met	Thr	His	Gly	Ala	Tyr	Lys	Val	Arg	Ile	Ala	Val	395	400	405
Leu	Ser	Asp	Gly	Thr	Leu	Asn	Phe	Thr	Asn	Val	Thr	Val	Gln	Asp	410	415	420
Thr	Gly	Met	Tyr	Thr	Cys	Met	Val	Ser	Asn	Ser	Val	Gly	Asn	Thr	425	430	435
Thr	Ala	Ser	Ala	Thr	Leu	Asn	Val	Thr	Ala	Ala	Thr	Thr	Thr	Pro	440	445	450
Phe	Ser	Tyr	Phe	Ser	Thr	Val	Thr	Val	Glu	Thr	Met	Glu	Pro	Ser	455	460	465
Gln	Asp	Glu	Ala	Arg	Thr	Thr	Asp	Asn	Asn	Val	Gly	Pro	Thr	Pro	470	475	480



Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro  
485 490 495

Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr  
500 505 510

Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr  
515 520 525

Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala  
530 535 540

Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His  
545 550 555

Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn  
560 565 570

Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu  
575 580 585

Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser  
590 595 600

Tyr Lys Ser Pro Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn  
605 610 615

Ser Ile His Ser Ser Val His Glu Pro Leu Leu Ile Arg Met Asn  
620 625 630

Ser Lys Asp Asn Val Gln Glu Thr Gln Ile  
635 640

<210> 502  
<211> 2458  
<212> DNA  
<213> Homo Sapien

<400> 502  
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cgcccggaac atggctgcag ccacctgcg cgcacccga ggcgcgcgc 100  
ccagctgcgc cgaggtccgt cggaggcgcc cggcgcccc ggagccaagc 150  
agcaactgag cggggaagcg cccgcgtccg gggatcgga tgctccctcc 200  
ccttctctc ttgctagttt cctactatgt tggaaccttg gggactcaca 250  
ctgagatcaa gagagtggca gaggaaaagg tcactttgcc ctgccaccat 300  
caactggggc ttccagaaaa agacactctg gatattgaat ggctgctcac 350  
cgataatgaa gggaacaaaa aagtgggtgat cacttactcc agtcgtcatg 400  
tctacaataa cttgactgag gaacagaagg gccgagtgcc ctttgcttcc 450  
aatttctctg caggagatgc ctccctgcag attgaacctc tgaagcccag 500  
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 aaccacacct gacgagttct gctgcagaat cttaccatgt cctactctgg 800  
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 tcgctccaca gcaaatagtg cctcagcgag ccagcgagca ctgtcaactg 1150  
 acgcagcacc ccagccaggg ctggccaccc aggcatacag ctagtgggg 1200  
 ccagagtgta gaggttctga accaaagaaa gtccaccatg ctaatctgac 1250  
 caaagcagaa accacacca gcatgatccc cagccagagc agagccttcc 1300  
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 gggctcttgg actcttctcg tcattggagc tcaagtcacc agccacacaa 1400  
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 gtatcagtg tttgattcac aattttcaag aggaaatggg atgctgtttg 1700  
 taaattttct atgcatttct gaaaacttat tggattatta gttattcaga 1750  
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 ctgacttaac ttcatttgct ataaggttg gatattaatt tcaaggggag 1900  
 ttgaaatagt gggagattga gaagagtga tgagtttct ccaactctata 1950  
 ctaattctac tatttgtatt gagccaaaa taactatgaa aggagacaaa 2000  
 aatttgtgac aaaggattgt gaagagcttt ccatcttcat gatgttatga 2050  
 ggattgttga caaacattag aaatatataa tggagcaatt gtggatttcc 2100  
 cctcaaatca gatgcctcta aggactttcc tgctagatat ttctggaagg 2150  
 agaaaaata acatgtcatt tatcaacgct ctagaaaga attctctag 2200

agaaaaaggg atctaggaat gctgaaagat tacccaacat accattatag 2250  
 tctcttcttt ctgagaaaa gtgaaaccag aattgcaaga ctgggtggac 2300  
 tagaaagggg gattagatca gttttctctt aatagtcaa ggaaggtagc 2350  
 cgggcatggg gccaggcacc ttaggaaaa tccagcaggt ggaggttgca 2400  
 gtgagccgag attatgccat tgcactccag cctgggtgac agagcggggac 2450  
 tccgtctc 2458

<210> 503

<211> 373

<212> PRT

<213> Homo Sapien

<400> 503

Met	Ser	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Val	Ser	Tyr	Tyr	Val	Gly
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Thr	Leu	Gly	Thr	His	Thr	Glu	Ile	Lys	Arg	Val	Ala	Glu	Glu	Lys
				20					25					30
Val	Thr	Leu	Pro	Cys	His	His	Gln	Leu	Gly	Leu	Pro	Glu	Lys	Asp
				35					40					45
Thr	Leu	Asp	Ile	Glu	Trp	Leu	Leu	Thr	Asp	Asn	Glu	Gly	Asn	Gln
				50					55					60
Lys	Val	Val	Ile	Thr	Tyr	Ser	Ser	Arg	His	Val	Tyr	Asn	Asn	Leu
				65					70					75
Thr	Glu	Glu	Gln	Lys	Gly	Arg	Val	Ala	Phe	Ala	Ser	Asn	Phe	Leu
				80					85					90
Ala	Gly	Asp	Ala	Ser	Leu	Gln	Ile	Glu	Pro	Leu	Lys	Pro	Ser	Asp
				95					100					105
Glu	Gly	Arg	Tyr	Thr	Cys	Lys	Val	Lys	Asn	Ser	Gly	Arg	Tyr	Val
				110					115					120
Trp	Ser	His	Val	Ile	Leu	Lys	Val	Leu	Val	Arg	Pro	Ser	Lys	Pro
				125					130					135
Lys	Cys	Glu	Leu	Glu	Gly	Glu	Leu	Thr	Glu	Gly	Ser	Asp	Leu	Thr
				140					145					150
Leu	Gln	Cys	Glu	Ser	Ser	Ser	Gly	Thr	Glu	Pro	Ile	Val	Tyr	Tyr
				155					160					165
Trp	Gln	Arg	Ile	Arg	Glu	Lys	Glu	Gly	Glu	Asp	Glu	Arg	Leu	Pro
				170					175					180
Pro	Lys	Ser	Arg	Ile	Asp	Tyr	Asn	His	Pro	Gly	Arg	Val	Leu	Leu
				185					190					195
Gln	Asn	Leu	Thr	Met	Ser	Tyr	Ser	Gly	Leu	Tyr	Gln	Cys	Thr	Ala
				200					205					210
Gly	Asn	Glu	Ala	Gly	Lys	Glu	Ser	Cys	Val	Val	Arg	Val	Thr	Val
				215					220					225

Gln Tyr Val Gln Ser Ile Gly Met Val Ala Gly Ala Val Thr Gly  
230 235 240

Ile Val Ala Gly Ala Leu Leu Ile Phe Leu Leu Val Trp Leu Leu  
245 250 255

Ile Arg Arg Lys Asp Lys Glu Arg Tyr Glu Glu Glu Arg Pro  
260 265 270

Asn Glu Ile Arg Glu Asp Ala Glu Ala Pro Lys Ala Arg Leu Val  
275 280 285

Lys Pro Ser Ser Ser Ser Ser Gly Ser Arg Ser Ser Arg Ser Gly  
290 295 300

Ser Ser Ser Thr Arg Ser Thr Ala Asn Ser Ala Ser Arg Ser Gln  
305 310 315

Arg Thr Leu Ser Thr Asp Ala Ala Pro Gln Pro Gly Leu Ala Thr  
320 325 330

Gln Ala Tyr Ser Leu Val Gly Pro Glu Val Arg Gly Ser Glu Pro  
335 340 345

Lys Lys Val His His Ala Asn Leu Thr Lys Ala Glu Thr Thr Pro  
350 355 360

Ser Met Ile Pro Ser Gln Ser Arg Ala Phe Gln Thr Val  
365 370

<210> 504  
<211> 3060  
<212> DNA  
<213> Homo Sapien

<400> 504  
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ctcctgtgcg gtagtagtga tttgccaga agtttgagta tcaactactc 150  
tgaagagatg attgaaaaag ccaaagggga aactgcctat ctgccatgca 200  
aatttacgct tagtcccga gaccagggac cgctggacat cgagtggctg 250  
atatcaccag ctgataatca gaaggtggat caagtgatta ttttatattc 300  
tggagacaaa atttatgatg actactatcc agatctgaaa ggccgagtac 350  
attttacgag taatgatctc aaatctgggtg atgcatcaat aaatgtaacg 400  
aatttacaac tgtcagatat tggcacatat cagtgcacaa tgaaaaaagc 450  
tcctgggtgtt gcaaaaaaga agattcatct ggtagtcttt gttaaagcctt 500  
caggtgcgag atgttacgtt gatggatctg aagaaattgg aagtgacttt 550  
aagataaaat gtgaacaaa agaaggttca cttccattac agtatgagtg 600  
gcaaaaattg totgactcac agaaaatgcc cacttcattg ttagcagaaa 650  
tgacttcac tgattatctc gtaaaaaatg cctcttctga gtactctggg 700

acatacagct gtacagtcag aaacagagtg ggctctgac agtgccgtgt 750  
 gcgtctaaac gttgtccctc cttcaaataa agctggacta attgcaggag 800  
 ccattatagg aactttgctt gctctagcgc tcatgtgtct tatcatcttt 850  
 tgctgtcgta aaaagcgcag agaagaaaaa tatgaaaagg aagttcatca 900  
 cgatatcagg gaagatgtgc caccctcaaa gagccgtacg tccactgcc 950  
 gaagctacat cggcagtaat cattcatccc tggggtccat gtctccttcc 1000  
 aacatggaag gatattccaa gactcagtat aaccaagtac caagtgaaga 1050  
 ctttgaacgc actcctcaga gtcgactct cccacctgct aagttcaagt 1100  
 acccttcaaa gactgatgga attacagttg tataaatatg gactactgaa 1150  
 gaatctgaag tattgtatta ttgacttta ttttaggctt ctagttaaaga 1200  
 cttaaatggt ttttaaaaa agcacaaggc acagagatta gagcagctgt 1250  
 aagaacacat ctactttatg caatggcatt agacatgtaa gtcagatgtc 1300  
 atgtcaaaat tagtacgagc caaattcttt gttaaaaaac cctatgtata 1350  
 gtgacactga tagttaaag atgttttatt atattttcaa taactaccac 1400  
 taacaaattt ttaacttttc atatgcata tctgatagt ggtcttttag 1450  
 gaaaagtatg gtaaatagtt gatttttcaa aggaattttt aaaattctta 1500  
 cgttctgttt aatgtttttg ctatttagtt aaatacattg aagggaata 1550  
 ccggttcttt tcccttttta tgcacacaac agaaacacgc gttgtcatgc 1600  
 ctcaaaactat tttttatttg caactacatg atttcacaca attctcttaa 1650  
 acaacgacat aaaatagatt tccttgata taaataaact acatacgctc 1700  
 cataaagtaa atttcaaaag gtgctagaac aaatcgtcca cttctacagt 1750  
 gttctcgtat ccaacagagt tgatgcacaa tatataaata ctcaagtcca 1800  
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 tatcaatata taaagtgcatt atatttttta agaaagatta ttctcaataa 1900  
 cttctataaa aataagtttg atggtttggc ccatctaact tcactactat 1950  
 tagtaagaac ttttaacttt taatgtgtag taaggtttat tctacctttt 2000  
 tctcaacatg acaccaacac aatcaaaaac gaagttagtg aggtgctaac 2050  
 atgtgaggat taatccagtg attccggtca caatgcattc caggaggagg 2100  
 taccatgtgc actggaattg ggcgatatgg tttatttttt cttccctgat 2150  
 ttggataacc aaatggaaca ggaggaggat agtgattctg atggccattc 2200  
 cctcgatata ttcttggtt ttttctgggc aaagggtgcc acattggaag 2250  
 aggtggaat ataagtctg aaatctgtag ggaagagaac acattaagtt 2300

aattcaaagg aaaaaatcat catctatgtt ccagatttct cattaagaac 2350  
aaagttacc acaacactga gatcacatct aagtgacact cctattgtca 2400  
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aggtgaccaa tgttttctga atgcataaag aaatgaataa actcaaacac 2500  
agtacttctt aaacaacttc aaccaaaaaa gaccaaaaaca tggaaacgaat 2550  
ggaagcttgt aaggacatgc ttgttttagt ccagtgtgtt ccacagctgg 2600  
ctaagccagg agtcacttgg aggcctttta atacaaaaca ttggagctgg 2650  
aggccattat ccttagcaaa ctaatgcaga aacagaaaaa caactaccgc 2700  
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gaaggaacaa atagacattg gagtctattt gagaggggag ggtgggagaa 2800  
ggaaaaggag cagaaaagat aactattgag tactgccttc acacctgggt 2850  
gatgaaataa tatgtacaac aaatccctgt gacacatgtt tacctatgga 2900  
acaaaccttc atgtgtatcc ctaaacctaa aataaaagtt aaaaaaaaaa 2950  
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aaaaaaaaaa 3060

<210> 505  
<211> 352  
<212> PRT  
<213> Homo Sapien

<400> 505  
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Phe Ala Arg Ser Leu Ser Ile Thr Thr Pro Glu Glu Met Ile Glu  
20 25 30  
Lys Ala Lys Gly Glu Thr Ala Tyr Leu Pro Cys Lys Phe Thr Leu  
35 40 45  
Ser Pro Glu Asp Gln Gly Pro Leu Asp Ile Glu Trp Leu Ile Ser  
50 55 60  
Pro Ala Asp Asn Gln Lys Val Asp Gln Val Ile Ile Leu Tyr Ser  
65 70 75  
Gly Asp Lys Ile Tyr Asp Asp Tyr Tyr Pro Asp Leu Lys Gly Arg  
80 85 90  
Val His Phe Thr Ser Asn Asp Leu Lys Ser Gly Asp Ala Ser Ile  
95 100 105  
Asn Val Thr Asn Leu Gln Leu Ser Asp Ile Gly Thr Tyr Gln Cys  
110 115 120  
Lys Val Lys Lys Ala Pro Gly Val Ala Asn Lys Lys Ile His Leu

	125		130		135
Val Val Leu Val Lys Pro Ser Gly Ala Arg Cys Tyr Val Asp Gly	140		145		150
Ser Glu Glu Ile Gly Ser Asp Phe Lys Ile Lys Cys Glu Pro Lys	155		160		165
Glu Gly Ser Leu Pro Leu Gln Tyr Glu Trp Gln Lys Leu Ser Asp	170		175		180
Ser Gln Lys Met Pro Thr Ser Trp Leu Ala Glu Met Thr Ser Ser	185		190		195
Val Ile Ser Val Lys Asn Ala Ser Ser Glu Tyr Ser Gly Thr Tyr	200		205		210
Ser Cys Thr Val Arg Asn Arg Val Gly Ser Asp Gln Cys Leu Leu	215		220		225
Arg Leu Asn Val Val Pro Pro Ser Asn Lys Ala Gly Leu Ile Ala	230		235		240
Gly Ala Ile Ile Gly Thr Leu Leu Ala Leu Ala Leu Ile Gly Leu	245		250		255
Ile Ile Phe Cys Cys Arg Lys Lys Arg Arg Glu Glu Lys Tyr Glu	260		265		270
Lys Glu Val His His Asp Ile Arg Glu Asp Val Pro Pro Pro Lys	275		280		285
Ser Arg Thr Ser Thr Ala Arg Ser Tyr Ile Gly Ser Asn His Ser	290		295		300
Ser Leu Gly Ser Met Ser Pro Ser Asn Met Glu Gly Tyr Ser Lys	305		310		315
Thr Gln Tyr Asn Gln Val Pro Ser Glu Asp Phe Glu Arg Thr Pro	320		325		330
Gln Ser Pro Thr Leu Pro Pro Ala Lys Phe Lys Tyr Pro Tyr Lys	335		340		345
Thr Asp Gly Ile Thr Val Val	350				

<210> 506  
 <211> 1705  
 <212> DNA  
 <213> Homo Sapien

<400> 506  
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 ccagctgcct ccaggcagcc agccctcaag catcacttac aggaccagag 150  
 ggacaagaca tgactgtgat gaggagctgc ttccgccaat ttaacaccaa 200  
 gaagaattga ggctgcttgg gaggaaggcc aggaggaaca cgagactgag 250

agatgaattt tcaacagagg ctgcaaagcc tgtggacttt agccagaccc 300  
 ttctgcctc ctttgcctgc gacagcctct caaatgcaga tggttgtgct 350  
 cccttgccct gggttttacc tgcttctctg gagccaggta tcagggggccc 400  
 agggccaaga attccacttt gggccctgcc aagtgaaggg ggtgttccc 450  
 cagaaactgt gggaagcctt ctgggctgtg aaagacacta tgcaagctca 500  
 ggataacatc acgagtgcgc ggctgctgca gcaggaggtt ctgcagaacg 550  
 tctcgtagtc tgagagctgt taccttgccc acaccctgct ggagttctac 600  
 ttgaaaactg ttttcaaaaa ccaccacaat agaacagttg aagtccaggac 650  
 tctgaagtca ttctctactc tggccaacaa ctttgttctc atcgtgtcac 700  
 aactgcaacc cagtcaagaa aatgagatgt tttccatcag agacagtgc 750  
 cacaggcggt ttctgctatt ccggagagca ttcaaacagt tggacgtaga 800  
 agcagctctg accaaagccc ttggggaagt ggacattctt ctgacctgga 850  
 tgcagaaatt ctacaagctc tgaatgtcta gaccaggacc tccctccccc 900  
 tggcactggt ttgtccctg tgcatttca aacagttctc cttctatgc 950  
 tgttcaactg acacttcacg cccttgccca tgggtcccat tcttgccca 1000  
 ggattattgt caaagaagtc attctttaag cagcgccagt gacagtcagg 1050  
 gaagggtgct ctggatgctg tgaagagtc acagagaaga ttcttgtatt 1100  
 tattacaact ctatttaatt aatgtcagta ttcaactga agttctatct 1150  
 atttgtgaga ctgtaagtta catgaaggca gcagaatatt gtgccccatg 1200  
 cttctttacc cctcacaatc ctgcccacag tgtggggcag tggatgggtg 1250  
 cttagtaagt acttaataaa ctgtggtgct ttttttggcc tgtctttgga 1300  
 ttgttaaaaa acagagaggg atgcttgat gtaaaactga acttcagagc 1350  
 atgaaaaatc cactgtcttc tgatatctgc agggacagag cattgggggtg 1400  
 ggggtaaggt gcatctgttt gaaaagtaaa cgataaaatg tggattaaag 1450  
 tggccagcac aaagcagatc ctcaataaac atttcatttc cccccacac 1500  
 tgcgcagctc accccatcat ccctttccct tgggtccctc cttttttttt 1550  
 tatctagtc attcttccct aatcttccac ttgagtgtca agctgacctt 1600  
 gctgatgggt acattgcacc tggatgtact atccaatctg tgatgacatt 1650  
 ccctgctaataaaaagacaacataactccaaaaaa 1700  
 aaaa 1705

<210> 507  
 <211> 206  
 <212> PRT



<213> Homo Sapien

<400> 507

Met	Asn	Phe	Gln	Gln	Arg	Leu	Gln	Ser	Leu	Trp	Thr	Leu	Ala	Arg
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Pro	Phe	Cys	Pro	Pro	Leu	Leu	Ala	Thr	Ala	Ser	Gln	Met	Gln	Met
				20					25					30
Val	Val	Leu	Pro	Cys	Leu	Gly	Phe	Thr	Leu	Leu	Trp	Ser	Gln	
				35					40					45
Val	Ser	Gly	Ala	Gln	Gly	Gln	Glu	Phe	His	Phe	Gly	Pro	Cys	Gln
				50					55					60
Val	Lys	Gly	Val	Val	Pro	Gln	Lys	Leu	Trp	Glu	Ala	Phe	Trp	Ala
				65					70					75
Val	Lys	Asp	Thr	Met	Gln	Ala	Gln	Asp	Asn	Ile	Thr	Ser	Ala	Arg
				80					85					90
Leu	Leu	Gln	Gln	Glu	Val	Leu	Gln	Asn	Val	Ser	Asp	Ala	Glu	Ser
				95					100					105
Cys	Tyr	Leu	Val	His	Thr	Leu	Leu	Glu	Phe	Tyr	Leu	Lys	Thr	Val
				110					115					120
Phe	Lys	Asn	His	His	Asn	Arg	Thr	Val	Glu	Val	Arg	Thr	Leu	Lys
				125					130					135
Ser	Phe	Ser	Thr	Leu	Ala	Asn	Asn	Phe	Val	Leu	Ile	Val	Ser	Gln
				140					145					150
Leu	Gln	Pro	Ser	Gln	Glu	Asn	Glu	Met	Phe	Ser	Ile	Arg	Asp	Ser
				155					160					165
Ala	His	Arg	Arg	Phe	Leu	Leu	Phe	Arg	Arg	Ala	Phe	Lys	Gln	Leu
				170					175					180
Asp	Val	Glu	Ala	Ala	Leu	Thr	Lys	Ala	Leu	Gly	Glu	Val	Asp	Ile
				185					190					195
Leu	Leu	Thr	Trp	Met	Gln	Lys	Phe	Tyr	Lys	Leu				
				200					205					

<210> 508

<211> 924

<212> DNA

<213> Homo Sapien

<400> 508

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cgggtctcagg agatgtctga ttccacaga catgcaccat atagaagaga 150  
gtttccaaga aatcaaaaga gccatccaag ctaaggacac cttccaaat 200  
gtcactatcc tgtccacatt ggagactctg cagatcatta agcccttaga 250  
tgtgtgctgc gtgaccaaga acctcctggc gttctacgtg gacagggtgt 300

tcaaggatca tcaggagcca aacccccaaa tcttgagaaa aatcagcagc 350  
attgccaaact ctttcctcta catgcagaaa actctgcggc aatgtcagga 400  
acagaggcag tgtcactgca ggcaggaagc caccaatgcc accagagtca 450  
tccatgacaa ctatgatcag ctggagggtcc acgctgctgc cattaaatcc 500  
ctgggagagc tcgacgtctt tctagcctgg attaataaga atcatgaagt 550  
aatgttctca gcttgatgac aaggaaacctg tatagtgatc cagggatgaa 600  
caccocctgt gcggtttact gtgggagaca gccacacctg aaggggaagg 650  
agatggggaa ggcoccttgc agctgaaagt cccactggct ggccacaggc 700  
tgtcttattc cgcttgaaaa taggcaaaaa gtctactgtg gtatttgtaa 750  
taaactctat ctgctgaaag ggcctgcagg ccactcctgg agtaaagggc 800  
tgccttccca tctaatttat tgtaaagtca tatagtccat gtctgtgatg 850  
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ataaattoca tattttacct atga 924

<210> 509

<211> 177

<212> PRT

<213> Homo Sapien

<400> 509

Met	Lys	Leu	Gln	Cys	Val	Ser	Leu	Trp	Leu	Leu	Gly	Thr	Ile	Leu	
1				5					10					15	
Ile	Leu	Cys	Ser	Val	Asp	Asn	His	Gly	Leu	Arg	Arg	Cys	Leu	Ile	
				20					25					30	
Ser	Thr	Asp	Met	His	His	Ile	Glu	Glu	Ser	Phe	Gln	Glu	Ile	Lys	
				35					40					45	
Arg	Ala	Ile	Gln	Ala	Lys	Asp	Thr	Phe	Pro	Asn	Val	Thr	Ile	Leu	
				50					55					60	
Ser	Thr	Leu	Glu	Thr	Leu	Gln	Ile	Ile	Lys	Pro	Leu	Asp	Val	Cys	
				65					70					75	
Cys	Val	Thr	Lys	Asn	Leu	Leu	Ala	Phe	Tyr	Val	Asp	Arg	Val	Phe	
				80					85					90	
Lys	Asp	His	Gln	Glu	Pro	Asn	Pro	Lys	Ile	Leu	Arg	Lys	Ile	Ser	
				95					100					105	
Ser	Ile	Ala	Asn	Ser	Phe	Leu	Tyr	Met	Gln	Lys	Thr	Leu	Arg	Gln	
				110					115					120	
Cys	Gln	Glu	Gln	Arg	Gln	Cys	His	Cys	Arg	Gln	Glu	Ala	Thr	Asn	
				125					130					135	
Ala	Thr	Arg	Val	Ile	His	Asp	Asn	Tyr	Asp	Gln	Leu	Glu	Val	His	
				140					145					150	
Ala	Ala	Ala	Ile	Lys	Ser	Leu	Gly	Glu	Leu	Asp	Val	Phe	Leu	Ala	

Trp Ile Asn Lys Asn His Glu Val Met Phe Ser Ala  
170 175

<210> 510  
<211> 996  
<212> DNA  
<213> Homo Sapien

<400> 510  
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cacatacgat ttaggtgaca ctatagaata acatccacctt tgccctttctc 150  
tccacaggtg tccactccca ggtccaactg cacctcggtt ctatcgataa 200  
tctcagcacc agccactcag agcagggcac gatgttgggg gcccgctca 250  
ggctctgggt ctgtgccttg tgcagcgtct gcagcatgag cgctctcaga 300  
gcctatccca atgcctcccc actgctcggc tccagctggg gtggcctgat 350  
ccacctgtac acagccacag ccaggaacag ctaccacctg cagatccaca 400  
agaatggcca tgtggatggc gcaccccatc agaccatcta cagtgccttg 450  
atgatcagat cagaggatgc tggctttgtg gtgattacag gtgtgatgag 500  
cagaagatac ctctgcatgg atttcagagg caacattttt ggatcacact 550  
atttcgaccg ggagaactgc aggttccaac accagacgct ggaaaacggg 600  
tacgacgtct accactctcc tcagtatcac ttctgggtca gtctgggccc 650  
ggcgaagaga gccttctctg caggcatgaa cccacccccg tactcccagt 700  
tcctgtcccc gaggaacgag atccccctaa ttcacttcaa ccccccata 750  
ccaacggcggc acacccggag cgcgaggac gactcggagc gggacccct 800  
gaacgtgctg aagccccggg cccggatgac cccggccccg gcctcctggt 850  
cacaggagct cccgagcgcc gaggacaaca gcccgatggc cagtgacca 900  
ttaggggttg tcaggggcgg tcgagtgaac acgcacgctg ggggaacggg 950  
cccgaaggc tgccgccccct tcgccaagtt catctagggt cgctgg 996

<210> 511  
<211> 251  
<212> PRT  
<213> Homo Sapien

<400> 511  
Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys Ser  
1 5 10 15  
Val Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro  
20 25 30

Leu Leu Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala  
 35 40  
 Thr Ala Arg Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His  
 50 55 60  
 Val Asp Gly Ala Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile  
 65 70 75  
 Arg Ser Glu Asp Ala Gly Phe Val Val Ile Thr Gly Val Met Ser  
 80 85 90  
 Arg Arg Tyr Leu Cys Met Asp Phe Arg Gly Asn Ile Phe Gly Ser  
 95 100 105  
 His Tyr Phe Asp Pro Glu Asn Cys Arg Phe Gln His Gln Thr Leu  
 110 115 120  
 Glu Asn Gly Tyr Asp Val Tyr His Ser Pro Gln Tyr His Phe Leu  
 125 130 135  
 Val Ser Leu Gly Arg Ala Lys Arg Ala Phe Leu Pro Gly Met Asn  
 140 145 150  
 Pro Pro Pro Tyr Ser Gln Phe Leu Ser Arg Arg Asn Glu Ile Pro  
 155 160 165  
 Leu Ile His Phe Asn Thr Pro Ile Pro Arg Arg His Thr Arg Ser  
 170 175 180  
 Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu Asn Val Leu Lys Pro  
 185 190 195  
 Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys Ser Gln Glu Leu  
 200 205 210  
 Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp Pro Leu Gly  
 215 220 225  
 Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly Thr Gly  
 230 235 240  
 Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile  
 245 250

<210> 512  
 <211> 2015  
 <212> DNA  
 <213> Homo Sapien

<400> 512  
 ggaaaaaggta ccgcgcagag acagccagca gttctgtgga gcagcgggtg 50  
 ccggctagga tgggctgtct ctggggtctg gctctgcccc tttttttt 100  
 ctgctgggag gttggggtct ctgggagctc tgcaggcccc agcaccgcga 150  
 gaggcagcac tgcgatgaca acggacgaca cagaagtgcc cgctatgact 200  
 ctaggaccgg gccacgccgc tctggaaact caaacgtcga gcgctgagac 250  
 ctcttctagg gctcaaccc cagccggccc cattccagaa gcagagacca 300

ggggagccaa gagaatttcc cctgcaagag agaccaggag ttccacaaaa 350  
 acatctccca acttcatggt gctgatcgcc acctccgtgg agacatcagc 400  
 cgccagtggc agccccgagg gagctggaat gaccacagtt cagaccatca 450  
 caggcagtga tcccagaggaa gccatctttg acaccctttg caccgatgac 500  
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 caccctocaca gaagctaagg gctgtcctc agagagcagt gcctcttccg 600  
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 tcttcgacg gcccccaccc agtcacaccc cgtcacggg cctcagagag 700  
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 cgggatctga tgtactctc ctgctgaag ccctggtgac tgcacaaaac 800  
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 ccacacatca ctgaggtcac agcctctgcc gagaccctgt ccacagccgg 1000  
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 agtggagctc tggtcacagt tagcaggaat ccctgggaag aaactcagc 1150  
 cctctctgtt gagacaccaa gttacgtcaa agtctcagga gcagctccgg 1200  
 tctccataga ggctgggtca gcagtgggca aaacaacttc ctttgcctgg 1250  
 agctctgctt cctcctacag cccctcggaa gccgcctca agaacttcac 1300  
 cccttcagag acaccgacca tggacatgc aaccaagggg ccctcccca 1350  
 ccagcagggc cctcttctc tctgtccctc cgactacaac caacagcagc 1400  
 cgagggacga acagcacctt agccaagatc acaacctcag cgaagaccac 1450  
 gatgaagccc caacagccac gccacgact gcccggaaga ggcgaccac 1500  
 agaagtgagt gcaggtgaaa atggagggtt cctcctcctg cggctgagt 1550  
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 cagcagctcc accgggaact ccacgcccac gcgcctcact tccaggtctc 1650  
 cttaactcgt gtcaggagag gctaacggac atcagctgca gccaggcatg 1700  
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 gggcagcatg tccaagcccc taacccaga tgtggcaaca ggacctcgc 1850  
 tcacatccac cggagtgtat gtatggggag gggcttcacc tgttccaga 1900

gggtgctcttg gactcacctt ggcacatggt ctgtgtttca gtaaagagag 1950  
 acctgatcac ccatctgtgt gcttccatcc tgcattaaaa ttactcagt 2000  
 gtggcccaaa aaaaa 2015

<210> 513  
 <211> 482  
 <212> PRT  
 <213> Homo Sapien

<400> 513  
 Met Gly Cys Leu Trp Gly Leu Ala Leu Pro Leu Phe Phe Phe Cys  
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 Trp Glu Val Gly Val Ser Gly Ser Ser Ala Gly Pro Ser Thr Arg  
 20 25 30  
 Arg Ala Asp Thr Ala Met Thr Thr Asp Asp Thr Glu Val Pro Ala  
 35 40 45  
 Met Thr Leu Ala Pro Gly His Ala Ala Leu Glu Thr Gln Thr Leu  
 50 55 60  
 Ser Ala Glu Thr Ser Ser Arg Ala Ser Thr Pro Ala Gly Pro Ile  
 65 70 75  
 Pro Glu Ala Glu Thr Arg Gly Ala Lys Arg Ile Ser Pro Ala Arg  
 80 85 90  
 Glu Thr Arg Ser Phe Thr Lys Thr Ser Pro Asn Phe Met Val Leu  
 95 100 105  
 Ile Ala Thr Ser Val Glu Thr Ser Ala Ala Ser Gly Ser Pro Glu  
 110 115 120  
 Gly Ala Gly Met Thr Thr Val Gln Thr Ile Thr Gly Ser Asp Pro  
 125 130 135  
 Glu Glu Ala Ile Phe Asp Thr Leu Cys Thr Asp Asp Ser Ser Glu  
 140 145 150  
 Glu Ala Lys Thr Leu Thr Met Asp Ile Leu Thr Leu Ala His Thr  
 155 160 165  
 Ser Thr Glu Ala Lys Gly Leu Ser Ser Glu Ser Ser Ala Ser Ser  
 170 175 180  
 Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg Ala Ser Glu Ser  
 185 190 195  
 Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg  
 200 205 210  
 Ala Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile  
 215 220 225  
 Thr Pro Ser Trp Ser Pro Gly Ser Asp Val Thr Leu Leu Ala Glu  
 230 235 240  
 Ala Leu Val Thr Val Thr Asn Ile Glu Val Ile Asn Cys Ser Ile  
 245 250 255

Thr	Glu	Ile	Glu	Thr	Thr	Thr	Ser	Ser	Ile	Pro	Gly	Ala	Ser	Asp	260	265	270
Ile	Asp	Leu	Ile	Pro	Thr	Glu	Gly	Val	Lys	Ala	Ser	Ser	Thr	Ser	275	280	285
Asp	Pro	Pro	Ala	Leu	Pro	Asp	Ser	Thr	Glu	Ala	Lys	Pro	His	Ile	290	295	300
Thr	Glu	Val	Thr	Ala	Ser	Ala	Glu	Thr	Leu	Ser	Thr	Ala	Gly	Thr	305	310	315
Thr	Glu	Ser	Ala	Ala	Pro	His	Ala	Thr	Val	Gly	Thr	Pro	Leu	Pro	320	325	330
Thr	Asn	Ser	Ala	Thr	Glu	Arg	Glu	Val	Thr	Ala	Pro	Gly	Ala	Thr	335	340	345
Thr	Leu	Ser	Gly	Ala	Leu	Val	Thr	Val	Ser	Arg	Asn	Pro	Leu	Glu	350	355	360
Glu	Thr	Ser	Ala	Leu	Ser	Val	Glu	Thr	Pro	Ser	Tyr	Val	Lys	Val	365	370	375
Ser	Gly	Ala	Ala	Pro	Val	Ser	Ile	Glu	Ala	Gly	Ser	Ala	Val	Gly	380	385	390
Lys	Thr	Thr	Ser	Phe	Ala	Gly	Ser	Ser	Ala	Ser	Ser	Tyr	Ser	Pro	395	400	405
Ser	Glu	Ala	Ala	Leu	Lys	Asn	Phe	Thr	Pro	Ser	Glu	Thr	Pro	Thr	410	415	420
Met	Asp	Ile	Ala	Thr	Lys	Gly	Pro	Phe	Pro	Thr	Ser	Arg	Asp	Pro	425	430	435
Leu	Pro	Ser	Val	Pro	Pro	Thr	Thr	Thr	Asn	Ser	Ser	Arg	Gly	Thr	440	445	450
Asn	Ser	Thr	Leu	Ala	Lys	Ile	Thr	Thr	Ser	Ala	Lys	Thr	Thr	Met	455	460	465
Lys	Pro	Gln	Gln	Pro	Arg	Pro	Arg	Leu	Pro	Gly	Arg	Gly	Arg	Pro	470	475	480
Gln	Thr																

<210> 514  
 <211> 2284  
 <212> DNA  
 <213> Homo Sapien

<400> 514  
 gcggagcatc cgctgcggtc ctgcgcgaga ccccccgcgcg gattcgcgcg 50  
 tccttcccgcc gggcgcgaca gagctgtcct cgcacctgga tggcagcagg 100  
 ggcgcgcgggg tcctctcgac gccagagaga aatctcatca tctgtgcagc 150  
 cttcttaaaag caaactaaga ccagagggag gattatcctt gacctttgaa 200  
 gacaaaaact aaactgaaat ttaaaatggt cttcggggga gaaggagact 250

tgacttacac tttggaata atttgcttcc tgacactaag gctgtctgct 300  
 agtcagaatt gcctcaaaaa gagtctagaa gatgttgtca ttgacatcca 350  
 gtcatctctt tctaagggaa tcagaggcaa tgagcccgta tatacttcaa 400  
 ctcaagaaga ctgcattaat tcttgctggt caacaaaaaa catatcaggg 450  
 gacaaagcat gtaacttgat gatcttcgac actcgaaaaa cagctagaca 500  
 acccaactgc tacctatctt totgtcccaa cgaggaagcc tgtccattga 550  
 aaccagcaaa aggacttatg agttacagga taattacaga tttccatct 600  
 ttgaccagaa atttgccaag ccaagagtta cccaggaag attctctctt 650  
 acatggccaa ttttcacaag cagtcactcc cctagcccat catcacacag 700  
 attattcaaa gccaccgat atctcatgga gagacacact ttctcagaag 750  
 tttggatcct cagatcacct ggagaaacta tttaagatgg atgaagcaag 800  
 tgcccgagctc cttgcttata aggaaaaagg ccattctcag agttcacaa 850  
 tttcctctga tcaagaaata gctcatctgc tgcccgaaaa tgtgagtgcg 900  
 ctcccgacta cgggtggcagt tgcttctcca cataccacct cggctactcc 950  
 aaagcccgcc acccttctac ccaccaatgc ttcagtgaca ccttctggga 1000  
 cttccagcc acagctggcc accacagctc cacctgtaac cactgtcact 1050  
 totcagcctc ccacgacct catttctaca gtttttacac gggtgcggc 1100  
 taactctcaa gcaatggcta caacagcagt tctgactacc acctttcag 1150  
 cacctacgga ctcgaaaggc agcttagaaa ccataccgtt tacagaaatc 1200  
 tccaacttaa ctttgaacac agggaaatgtg tataacccta ctgcactttc 1250  
 tatgtcaaat gtggagtctt ccactatgaa taaaactgct tctggggaag 1300  
 gtaggaggcc cagtcaggc agttcctccc agggcagtg tccagaaaat 1350  
 cagtcaggcc ttccatttga aaaatggctt cttatcgggt cctgctctt 1400  
 tgggtgctcg ttcttggtga taggcctcgt cctcctgggt agaatcctt 1450  
 cggaaatcact ccgcaggaaa cgttactcaa gactggatta ttgatcaat 1500  
 gggatctatg tggacatcta aggatggaac tcggtgtctc ttaattoatt 1550  
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 agcaggagggt tgtattttga agacaggaaa atgccccctt ctgctttcct 1650  
 tttttttttt ggagacagag tcttgctctg ttgccaggc tggagtgcag 1700  
 tagcacgato tcggctctca ccgcaacctc cgtctcctgg gttcaagcga 1750  
 ttctcctgcc tcagcctcct aagtatctgg gattacaggc atgtgccacc 1800  
 acacctgggt gatttttga ttttttagtag agacgggggt tcaccatggt 1850



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 cccaaagtgc tgggattaca ggcatgagcc accacagctg gccccttct 1950  
 gttttatgtt tgggttttga gaaggaatga agtgggaacc aaattaggta 2000  
 attttgggta atctgtctct aaaatattag ctaaaaaaa agctctatgt 2050  
 aaagtaataa agtataattg ccatataaat ttcaaaattc aactggcctt 2100  
 tatgcaaaga aacaggttag gacatctagg ttccaaattca ttcacattct 2150  
 tggttccaga taaaatcaac tgtttatatc aatttctaag ggatttgctt 2200  
 ttctttttat atggattcct ttaaaactta ttccagatgt agttccttcc 2250  
 aattaaatat ttgaataaat cttttgttac tcaa 2284

<210> 515  
 <211> 431  
 <212> PRT  
 <213> Homo Sapien

<400> 515  
 Met Phe Phe Gly Gly Glu Gly Ser Leu Thr Tyr Thr Leu Val Ile  
 1 5 10 15  
 Ile Cys Phe Leu Thr Leu Arg Leu Ser Ala Ser Gln Asn Cys Leu  
 20 25 30  
 Lys Lys Ser Leu Glu Asp Val Val Ile Asp Ile Gln Ser Ser Leu  
 35 40 45  
 Ser Lys Gly Ile Arg Gly Asn Glu Pro Val Tyr Thr Ser Thr Gln  
 50 55 60  
 Glu Asp Cys Ile Asn Ser Cys Cys Ser Thr Lys Asn Ile Ser Gly  
 65 70 75  
 Asp Lys Ala Cys Asn Leu Met Ile Phe Asp Thr Arg Lys Thr Ala  
 80 85 90  
 Arg Gln Pro Asn Cys Tyr Leu Phe Phe Cys Pro Asn Glu Glu Ala  
 95 100 105  
 Cys Pro Leu Lys Pro Ala Lys Gly Leu Met Ser Tyr Arg Ile Ile  
 110 115 120  
 Thr Asp Phe Pro Ser Leu Thr Arg Asn Leu Pro Ser Gln Glu Leu  
 125 130 135  
 Pro Gln Glu Asp Ser Leu Leu His Gly Gln Phe Ser Gln Ala Val  
 140 145 150  
 Thr Pro Leu Ala His His His Thr Asp Ser Lys Pro Thr Asp  
 155 160 165  
 Ile Ser Trp Arg Asp Thr Leu Ser Gln Lys Phe Gly Ser Ser Asp  
 170 175 180  
 His Leu Glu Lys Leu Phe Lys Met Asp Glu Ala Ser Ala Gln Leu  
 185 190 195

Leu Ala Tyr Lys Glu Lys Gly His Ser Gln Ser Ser Gln Phe Ser  
 200 205 210  
 Ser Asp Gln Glu Ile Ala His Leu Leu Pro Glu Asn Val Ser Ala  
 215 220 225  
 Leu Pro Ala Thr Val Ala Val Ala Ser Pro His Thr Thr Ser Ala  
 230 235 240  
 Thr Pro Lys Pro Ala Thr Leu Leu Pro Thr Asn Ala Ser Val Thr  
 245 250 255  
 Pro Ser Gly Thr Ser Gln Pro Gln Leu Ala Thr Thr Ala Pro Pro  
 260 265 270  
 Val Thr Thr Val Thr Ser Gln Pro Pro Thr Thr Leu Ile Ser Thr  
 275 280 285  
 Val Phe Thr Arg Ala Ala Ala Thr Leu Gln Ala Met Ala Thr Thr  
 290 295 300  
 Ala Val Leu Thr Thr Thr Phe Gln Ala Pro Thr Asp Ser Lys Gly  
 305 310 315  
 Ser Leu Glu Thr Ile Pro Phe Thr Glu Ile Ser Asn Leu Thr Leu  
 320 325 330  
 Asn Thr Gly Asn Val Tyr Asn Pro Thr Ala Leu Ser Met Ser Asn  
 335 340 345  
 Val Glu Ser Ser Thr Met Asn Lys Thr Ala Ser Trp Glu Gly Arg  
 350 355 360  
 Glu Ala Ser Pro Gly Ser Ser Ser Gln Gly Ser Val Pro Glu Asn  
 365 370 375  
 Gln Tyr Gly Leu Pro Phe Glu Lys Trp Leu Leu Ile Gly Ser Leu  
 380 385 390  
 Leu Phe Gly Val Leu Phe Leu Val Ile Gly Leu Val Leu Leu Gly  
 395 400 405  
 Arg Ile Leu Ser Glu Ser Leu Arg Arg Lys Arg Tyr Ser Arg Leu  
 410 415 420  
 Asp Tyr Leu Ile Asn Gly Ile Tyr Val Asp Ile  
 425 430

<210> 516  
 <211> 2749  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> unsure  
 <222> 1869, 1887  
 <223> unknown base

<400> 516  
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gcgggttcga aggggacact gtgtccctgc agtgcaccta caggggaagag 150  
 ctgaggggacc accggaagta ctggtgcagg aaggggtgga tctctttctc 200  
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 agggcagggt gtccatccgt gacagccgcc aggagctctc gctcattgtg 300  
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 cgaaaaacgg ggcgccgatg agtctttact gatctctctg ttctctttc 400  
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 acaacacgcc tgcagcccaa ggcaaaagct cagcaaaccc agccccagg 500  
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 cagtgaagca gtatggctg ctggatcagc accgattccc gaaagcttct 1100  
 cacctcagcc tcagagtcca gctgcccgga ctccagggct ctccccacc 1150  
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 agccctggag ccagagcggc tggccttgct ctccggctg gagactggga 1250  
 catccctgat aggttcacat cctgggagc agtaccaggc tgctgacct 1300  
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<210> 517

<211> 332

<212> PRT

<213> Homo Sapien

<400> 517

Met	Arg	Leu	Val	Leu	Leu	Trp	Gly	Cys	Leu	Leu	Leu	Pro	Gly
1				5				10					15
Tyr	Glu	Ala	Leu	Glu	Gly	Pro	Glu	Glu	Ile	Ser	Gly	Phe	Glu
				20					25				30
Asp	Thr	Val	Ser	Leu	Gln	Cys	Thr	Tyr	Arg	Glu	Glu	Leu	Arg
				35					40				45
His	Arg	Lys	Tyr	Trp	Cys	Arg	Lys	Gly	Gly	Ile	Leu	Phe	Ser
				50					55				60
Cys	Ser	Gly	Thr	Ile	Tyr	Ala	Glu	Glu	Glu	Gly	Gln	Glu	Thr
				65					70				75

Lys	Gly	Arg	Val	Ser	Ile	Arg	Asp	Ser	Arg	Gln	Glu	Leu	Ser	Leu	
				80					85					90	
Ile	Val	Thr	Leu	Trp	Asn	Leu	Thr	Leu	Gln	Asp	Ala	Gly	Glu	Tyr	
				95					100					105	
Trp	Cys	Gly	Val	Glu	Lys	Arg	Gly	Pro	Asp	Glu	Ser	Leu	Leu	Ile	
				110					115					120	
Ser	Leu	Phe	Val	Phe	Pro	Gly	Pro	Cys	Cys	Pro	Pro	Ser	Pro	Ser	
				125					130					135	
Pro	Thr	Phe	Gln	Pro	Leu	Ala	Thr	Thr	Arg	Leu	Gln	Pro	Lys	Ala	
				140					145					150	
Lys	Ala	Gln	Gln	Thr	Gln	Pro	Pro	Gly	Leu	Thr	Ser	Pro	Gly	Leu	
				155					160					165	
Tyr	Pro	Ala	Ala	Thr	Thr	Ala	Lys	Gln	Gly	Lys	Thr	Gly	Ala	Glu	
				170					175					180	
Ala	Pro	Pro	Leu	Pro	Gly	Thr	Ser	Gln	Tyr	Gly	His	Glu	Arg	Thr	
				185					190					195	
Ser	Gln	Tyr	Thr	Gly	Thr	Ser	Pro	His	Pro	Ala	Thr	Ser	Pro	Pro	
				200					205					210	
Ala	Gly	Ser	Ser	Arg	Pro	Pro	Met	Gln	Leu	Asp	Ser	Thr	Ser	Ala	
				215					220					225	
Glu	Asp	Thr	Ser	Pro	Ala	Leu	Ser	Ser	Gly	Ser	Ser	Lys	Pro	Arg	
				230					235					240	
Val	Ser	Ile	Pro	Met	Val	Arg	Ile	Leu	Ala	Pro	Val	Leu	Val	Leu	
				245					250					255	
Leu	Ser	Leu	Leu	Ser	Ala	Ala	Gly	Leu	Ile	Ala	Phe	Cys	Ser	His	
				260					265					270	
Leu	Leu	Leu	Trp	Arg	Lys	Glu	Ala	Gln	Gln	Ala	Thr	Glu	Thr	Gln	
				275					280					285	
Arg	Asn	Glu	Lys	Phe	Trp	Leu	Ser	Arg	Leu	Thr	Ala	Glu	Glu	Lys	
				290					295					300	
Glu	Ala	Pro	Ser	Gln	Ala	Pro	Glu	Gly	Asp	Val	Ile	Ser	Met	Pro	
				305					310					315	
Pro	Leu	His	Thr	Ser	Glu	Glu	Glu	Leu	Gly	Phe	Ser	Lys	Phe	Val	
				320					325					330	

Ser Ala

<210> 518

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 518

ccctgcagtg cacctacagg gaag 24

<210> 519

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

ctgtettccc ctgcttggt gtgg 24

<210> 520

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 520

ggtgcaggaa ggggtgggac ctcttctctc gctgctctgg ccacac 47

<210> 521

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 521

ccagtgcaca gcaggcaacg aagc 24

<210> 522

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 522

actaggctgt atgcctgggt gggc 24

<210> 523

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 523

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<210> 524

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe  
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 aatctcagca ccagccactc agagca 26  
 <210> 525  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic oligonucleotide probe  
 <400> 525  
 gttaaagagg gtgcccttcc agcga 25  
 <210> 526  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
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 <223> Synthetic oligonucleotide probe  
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 tatcccaatg cctccccact gctc 24  
 <210> 527  
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